



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140715

TO: Nita M Minnifield
Location: REM-3C01/3C18
Art Unit: 1645
Wednesday, December 22, 2004
Case Serial Number: 109/337584

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Minnifield,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

*Reviewed
12/30/04
mm*



STIC-Biotech/ChemLib

140715

From: Chan, Christina
Sent: Sunday, December 19, 2004 1:40 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush sequence search

Importance: High

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Sunday, December 19, 2004 1:39 PM
To: Chan, Christina
Subject: rush sequence search

Christina, please approve, 2 month amdt. due

STIC

09/337584

Please do a commercial and interference sequence search on
SEQ ID NO: 3, 7, 10, 12, 38 and 57 of this application.

Please provide a paper copy of all results.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 12/22
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgttctgatgct 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

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7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR140444 Sequence
2	20	100.0	20	6	AR140486 Sequence
3	20	100.0	20	6	AR146337 Sequence
4	20	100.0	20	6	AR14674 Sequence
5	20	100.0	20	6	BD205559 Method of
6	20	100.0	20	6	BD261101 Methods a
7	20	100.0	20	6	BD261264 Methods a
8	20	100.0	20	6	BD267868 Methods f
9	20	100.0	20	6	BD270770 Stereoiso
10	20	100.0	20	6	AR213843 Sequence
11	20	100.0	20	6	AR222210 Sequence
12	20	100.0	20	6	AR352589 Sequence
13	20	100.0	20	6	AR432426 Sequence
14	20	100.0	20	6	AX104585 Sequence
15	20	100.0	20	6	AX105178 Sequence
16	20	100.0	20	6	AX351748 Sequence
17	20	100.0	20	6	AX351814 Sequence
18	20	100.0	20	6	AX351837 Sequence
19	20	100.0	20	6	AX351865 Sequence

20	20	100.0	20	6	AX351886	Sequence
21	20	100.0	20	6	AX351911	Sequence
22	20	100.0	20	6	AX355517	Sequence
23	20	100.0	20	6	AX455600	Sequence
24	20	100.0	20	6	AX465343	Sequence
25	20	100.0	20	6	AX547638	Sequence
26	20	100.0	20	6	AX786552	Sequence
27	20	100.0	20	6	BD009051	Immunost
28	20	100.0	20	6	AX351932	Sequence
29	20	100.0	26	6	AX351755	Sequence
30	20	100.0	28	6	AX351953	Sequence
31	19	95.0	20	6	BD233633	Immunost
32	18.4	92.0	20	6	A89782	Sequence 4
33	18.4	92.0	20	6	A89783	Sequence 5
34	18.4	92.0	20	6	A90869	Sequence 4
35	18.4	92.0	20	6	A90870	Sequence 5
36	18.4	92.0	20	6	A93512	Sequence 5
37	18.4	92.0	20	6	A93521	Sequence 14
38	18.4	92.0	20	6	AR078394	Sequence
39	18.4	92.0	20	6	AR096710	Sequence
40	18.4	92.0	20	6	AR135054	Sequence
41	18.4	92.0	20	6	AR140448	Sequence
42	18.4	92.0	20	6	AR140476	Sequence
43	18.4	92.0	20	6	AR140485	Sequence
44	18.4	92.0	20	6	AR140495	Sequence
45	18.4	92.0	20	6	AR146312	Sequence

ALIGNMENTS

RESULT 1
AR140444
LOCUS AR140444 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 3 from patent US 6207646.
ACCESSION AR140444
VERSION AR140444.1 GI:14482940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6207646-A 3 27-MAR-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATAACGTTCTCTGATGCT 20
|||||
Db 1 TCCATAACGTTCTCTGATGCT 20

RESULT 2

AR140486
LOCUS AR140486 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 45 from patent US 6207646.
ACCESSION AR140486
VERSION AR140486.1 GI:14482982
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
TITLE Immunostimulatory nucleic acid molecules

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OM nucleic - nucleic search, using sw model
Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-3
Perfect score: 20
Sequence: 1 tccataacgttcctgatgct 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2 AAV27642	AAV27642 Immunosti
2	20	100.0	20	2 AAV27670	AAV27670 Immunosti
3	20	100.0	20	2 AAV27709	AAV27709 Immunosti
4	20	100.0	20	2 AAV27652	AAV27652 Immunosti
5	20	100.0	20	2 AAV80113	AAV80113 Oligo use
6	20	100.0	20	2 AAZ41895	Aaz41895 IL-12 sec
7	20	100.0	20	3 AAZ241895	Aaz60967 Nucleotid
8	20	100.0	20	3 AAZ47971	Aaz47971 Immune re
9	20	100.0	20	3 AAZ47842	Aaz47842 Immunosti
10	20	100.0	20	3 AAZ47835	Aaz47835 Parasitic
11	20	100.0	20	4 AAH50573	Aah50573 Mouse li-
12	20	100.0	20	4 AAH19253	Aah19253 Phosphodi
13	20	100.0	20	4 AAH19295	Aah19295 CpG Oligo
14	20	100.0	20	4 AAF98799	Aaf98799 CpG immu
15	20	100.0	20	4 AAF99577	Aaf99577 Immunosti
16	20	100.0	20	6 ABL35136	ABL35136 Immunosti
17	20	100.0	20	6 ABL35221	ABL35221 Immunosti
18	20	100.0	20	6 ABL35289	ABL35289 Immunosti
19	20	100.0	20	6 ABL35247	ABL35247 Immunosti
20	20	100.0	20	6 ABL35200	ABL35200 Immunosti
21	20	100.0	20	6 ABL35266	ABL35266 Immunosti

ALIGNMENTS

22	20	100.0	20	6 ABS78293	ABs78293 Angiogene
23	20	100.0	20	6 ABL39123	ABl39123 Immunosti
24	20	100.0	20	6 ABK46421	ABk46421 Immunosti
25	20	100.0	20	6 AAL39202	AAl39202 Murine To
26	20	100.0	20	6 ABS70555	ABs70555 Dendritic
27	20	100.0	20	9 ACA92700	ACa92700 Immunosti
28	20	100.0	20	9 ACD91401	ACd91401 Immunosti
29	20	100.0	20	9 ACH03115	ACH03115 Immunosti
30	20	100.0	20	9 ADB37079	ADb37079 Immunosti
31	20	100.0	20	10 AAD60205	AAd60205 Oligonuc
32	20	100.0	20	10 ADF09184	ADf09184 Immunomod
33	20	100.0	20	10 ADG68105	ADg68105 Unmethyla
34	20	100.0	20	10 ACF36783	ACf36783 Immunosti
35	20	100.0	20	10 ABX76032	ABx76032 Immunosti
36	20	100.0	20	10 ACAS8697	ACa58697 Gastric u
37	20	100.0	20	12 ADI01045	ADi01045 Immunosti
38	20	100.0	20	12 ADM99014	ADm99014 Immunosti
39	20	100.0	20	12 ADO04730	ADo04730 CpG oligo
40	20	100.0	20	12 ADQ07464	ADq07464 Immunosti
41	20	100.0	24	6 ABL35310	ABl35310 Immunosti
42	20	100.0	26	6 ABL35143	ABl35143 Immunosti
43	20	100.0	28	6 ABL35331	ABl35331 Immunosti
44	19.2	96.0	20	12 ADJ64048	ADj64048 oligonuc
45	19	95.0	20	3 AAZ55883	Aaz55883 Immunomod

RESULT 1
AAV27642
ID AAV27642 standard; DNA; 20 BP.
XX
AC AAV27642;
XX
DT 01-OCT-1998 (first entry)
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
FN WO9818810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US019791.
XX
PR 30-OCT-1996; 96US-00738652.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Kline JN;
XX
DR WPI, 1998-272127/24.
XX
DR New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections or autoimmune disease.
PT
PT Claim 23; Page 82; 109pp; English.
PS
XX
XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N1 is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tcataacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-08-738-652-3
2	20	100.0	20	3	US-08-738-652-3
3	20	100.0	20	3	US-08-738-652-3
4	20	100.0	20	3	US-08-738-652-3
5	20	100.0	20	3	US-08-738-652-3
6	20	100.0	20	3	US-08-738-652-3
7	20	100.0	20	3	US-08-738-652-3
8	20	100.0	20	3	US-08-738-652-3
9	18.4	92.0	20	3	US-08-738-652-3
10	18.4	92.0	20	3	US-08-738-652-3
11	18.4	92.0	20	3	US-08-738-652-3
12	18.4	92.0	20	3	US-08-738-652-3
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17	18.4	92.0	20	3	US-08-738-652-3
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19	18.4	92.0	20	3	US-08-738-652-3
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24	18.4	92.0	20	3	US-08-738-652-3
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26	18.4	92.0	20	3	US-08-738-652-3
27	18.4	92.0	20	3	US-08-738-652-3

28 18.4 92.0 20 4 US-09-337-619-7 Sequence 7, Appli
29 18.4 92.0 29 4 US-08-848-229-2 Sequence 2, Appli
30 18.4 92.0 29 4 US-09-022-965-2 Sequence 2, Appli
31 17.4 87.0 20 4 US-09-296-477-19 Sequence 19, Appli
32 16.8 84.0 20 3 US-08-738-652-9 Sequence 9, Appli
33 16.8 84.0 20 3 US-08-738-652-40 Sequence 40, Appli
34 16.8 84.0 20 3 US-08-738-652-43 Sequence 43, Appli
35 16.8 84.0 20 3 US-08-738-652-46 Sequence 46, Appli
36 16.8 84.0 20 3 US-08-738-652-47 Sequence 47, Appli
37 16.8 84.0 20 3 US-08-738-652-53 Sequence 53, Appli
38 16.8 84.0 20 3 US-09-030-701-5 Sequence 5, Appli
39 16.8 84.0 20 3 US-09-286-098-45 Sequence 45, Appli
40 16.8 84.0 20 3 US-09-286-098-48 Sequence 48, Appli
41 16.8 84.0 20 3 US-09-286-098-50 Sequence 50, Appli
42 16.8 84.0 20 3 US-09-286-098-51 Sequence 51, Appli
43 16.8 84.0 20 3 US-09-286-098-56 Sequence 56, Appli
44 16.8 84.0 20 3 US-09-286-098-57 Sequence 57, Appli
45 16.8 84.0 20 3 US-08-960-774-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-738-652-3
; Sequence 3, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-3

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATAACGTTCTCTGATGCT 20
|||
Db 1 TCATAACGTTCTCTGATGCT 20

RESULT 2

US-08-738-652-45
; Sequence 45, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tcataacggtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-09-824-468-49
2	20	100.0	20	9	US-09-800-266A-43
3	20	100.0	20	9	US-09-895-007A-43
4	20	100.0	20	9	US-09-920-313-43
5	20	100.0	20	10	US-09-888-326-545
6	20	100.0	20	10	US-09-818-918-3
7	20	100.0	20	10	US-09-818-918-45
8	20	100.0	20	10	US-09-931-583-42
9	20	100.0	20	10	US-09-776-479-777
10	20	100.0	20	10	US-09-954-987B-77
11	20	100.0	20	11	US-09-874-991C-44
12	20	100.0	20	11	US-09-874-991C-110

13	20	100.0	20	11	US-09-874-991C-133	Sequence 133, App
14	20	100.0	20	11	US-09-874-991C-161	Sequence 161, App
15	20	100.0	20	11	US-09-874-991C-182	Sequence 182, App
16	20	100.0	20	11	US-09-874-991C-207	Sequence 207, App
17	20	100.0	20	11	US-09-776-479-777	Sequence 777, App
18	20	100.0	20	13	US-10-023-909A-43	Sequence 43, Appl
19	20	100.0	20	14	US-10-112-653-750	Sequence 750, App
20	20	100.0	20	14	US-10-017-995-777	Sequence 777, App
21	20	100.0	20	14	US-10-300-247-43	Sequence 43, Appl
22	20	100.0	20	15	US-10-161-229-44	Sequence 44, Appl
23	20	100.0	20	15	US-10-187-264A-3	Sequence 3, Appli
24	20	100.0	20	15	US-10-265-072-78	Sequence 78, Appl
25	20	100.0	20	15	US-10-306-522-3	Sequence 3, Appli
26	20	100.0	20	15	US-10-314-578-777	Sequence 777, App
27	20	100.0	20	15	US-10-434-696-43	Sequence 43, Appl
28	20	100.0	20	16	US-10-373-381-36	Sequence 36, Appl
29	20	100.0	20	16	US-10-719-493-3	Sequence 3, Appli
30	20	100.0	20	17	US-10-627-331-3	Sequence 3, Appli
31	20	100.0	20	17	US-10-666-733-43	Sequence 43, Appl
32	20	100.0	20	17	US-10-743-625-3	Sequence 3, Appli
33	20	100.0	20	17	US-10-743-625-45	Sequence 45, Appl
34	20	100.0	20	17	US-10-769-282-3	Sequence 3, Appli
35	20	100.0	20	17	US-10-769-282-45	Sequence 45, Appl
36	20	100.0	20	18	US-10-817-165-3	Sequence 3, Appli
37	20	100.0	20	18	US-10-817-165-45	Sequence 45, Appl
38	20	100.0	20	18	US-10-877-407-33	Sequence 33, Appl
39	20	100.0	20	18	US-10-816-220-43	Sequence 43, Appl
40	20	100.0	20	18	US-10-831-778-777	Sequence 777, App
41	20	100.0	20	18	US-10-876-892-36	Sequence 36, Appl
42	20	100.0	20	18	US-10-876-965-36	Sequence 36, Appl
43	20	100.0	20	18	US-10-877-369-36	Sequence 36, Appl
44	20	100.0	20	24	US-09-874-991C-228	Sequence 228, App
45	20	100.0	26	11	US-09-874-991C-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-824-468-49
; Sequence 49, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the Immune System Using Immunotherapeutic Oligonucleotides and Cytokines
; TITLE OF INVENTION: Immune System
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-49

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAACGTTCTCTGATGCT 20

Db 1 TCATAACGTTCTCTGATGCT 20

RESULT 2

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	287	2	BF713668
2	18.4	92.0	648	6	CB176176
3	17.4	87.0	425	9	BX001224
4	17.4	87.0	855	7	CF932497
5	17.4	87.0	922	9	CNS01020
6	17.4	85.0	253	2	BB385734
7	16.8	84.0	158	2	BE164373
8	16.8	84.0	175	2	BB600645
9	16.8	84.0	217	9	CL808914
10	16.8	84.0	263	4	BG993633
11	16.8	84.0	341	2	BF457455
12	16.8	84.0	356	5	BP013861
13	16.8	84.0	365	1	AV962971
14	16.8	84.0	396	2	AW379917
15	16.8	84.0	424	5	BY241143
16	16.8	84.0	429	1	AU288167
17	16.8	84.0	429	1	AU288168
18	16.8	84.0	452	8	AZ162948
19	16.8	84.0	467	1	AI047174
20	16.8	84.0	472	1	AJ449482
21	16.8	84.0	496	1	AV675486
22	16.8	84.0	509	5	BW268112
23	16.8	84.0	510	8	AQ683537
24	16.8	84.0	511	8	BH394304

25	16.8	84.0	526	8	BH393114
26	16.8	84.0	545	1	AV989385
27	16.8	84.0	556	1	AV997839
28	16.8	84.0	556	4	BI540503
29	16.8	84.0	556	8	BH395140
30	16.8	84.0	585	1	AV997837
31	16.8	84.0	587	9	CG793447
32	16.8	84.0	591	1	AJ453167
33	16.8	84.0	594	1	AJ454344
34	16.8	84.0	598	1	AJ452440
35	16.8	84.0	598	9	CE030744
36	16.8	84.0	614	1	AJ447301
37	16.8	84.0	617	5	BW347030
38	16.8	84.0	631	5	BP184578
39	16.8	84.0	638	1	AI981577
40	16.8	84.0	646	4	BM485876
41	16.8	84.0	650	8	BH375955
42	16.8	84.0	657	8	BH404989
43	16.8	84.0	658	8	BH381954
44	16.8	84.0	666	7	CK834056
45	16.8	84.0	667	2	BB630476

ALIGNMENTS

RESULT 1
BF713668
LOCUS
DEFINITION
ESTPBL223 differential display RT-PCR clones Sus scrofa cDNA clone
BL223, mRNA sequence.
ACCESSION
BF713668
VERSION
BF713668.1
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
REFERENCE
1 (bases 1 to 287)
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS
Ponsuksilli, S., Wimmers, K. and Schellander, K.
TITLE
Identification of porcine liver ESTs by differential display RT-PCR
JOURNAL
Unpublished (2001)
COMMENT
Contact: Ponsuksilli S
Institute of Animal Breeding Science
University of Bonn
Endenicher Allee 15, Bonn 53115, Germany
Seq primer: T7 Sp6
High quality sequence stop: 287
POLYA=No.

FEATURES
Location/Qualifiers
1..287
Source
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="BL223"
/note="Organ: liver; CDNA fragments obtained from differential display RT-PCR banding patterns were cloned into pGEM"

ORIGIN

Query Match
Best Local Similarity 92.0%; Score 18.4; DB 2; Length 287;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTAACGTTCTCTGATGCT 20

Dd 14 TCCTAGCGTTCTCTGATGCT 33

RESULT 2

CB176176

LOCUS
CB176176 648 bp mRNA linear EST 31-JAN-2003

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttccctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	A89782 Sequence 4
2	20	100.0	20	6	A89783 Sequence 5
3	20	100.0	20	6	A90869 Sequence 4
4	20	100.0	20	6	A90870 Sequence 5
5	20	100.0	20	6	A93512 Sequence 5
6	20	100.0	20	6	A93521 Sequence 14
7	20	100.0	20	6	AR078394 Sequence
8	20	100.0	20	6	AR096710 Sequence
9	20	100.0	20	6	AR135054 Sequence
10	20	100.0	20	6	AR140448 Sequence
11	20	100.0	20	6	AR140476 Sequence
12	20	100.0	20	6	AR140485 Sequence
13	20	100.0	20	6	AR140495 Sequence
14	20	100.0	20	6	AR146312 Sequence
15	20	100.0	20	6	AR154678 Sequence
16	20	100.0	20	6	BD190423 Microemul
17	20	100.0	20	6	BD205534 Method of
18	20	100.0	20	6	BD251271 Enhanceme
19	20	100.0	20	6	BD261076 Methods a

20	20	100.0	20	6	BD261240	Methods a
21	20	100.0	20	6	BD261564	Vaccine.
22	20	100.0	20	6	BD267846	Methods f
23	20	100.0	20	6	BD270746	Stereoiso
24	20	100.0	20	6	CQ788117	Sequence
25	20	100.0	20	6	CQ788203	Sequence
26	20	100.0	20	6	CQ798386	Sequence
27	20	100.0	20	6	CQ812848	Sequence
28	20	100.0	20	6	CQ815139	Sequence
29	20	100.0	20	6	CQ829543	Sequence
30	20	100.0	20	6	AR182896	Sequence
31	20	100.0	20	6	AR182907	Sequence
32	20	100.0	20	6	AR213827	Sequence
33	20	100.0	20	6	AR222199	Sequence
34	20	100.0	20	6	AR237032	Sequence
35	20	100.0	20	6	AR237039	Sequence
36	20	100.0	20	6	AR303122	Sequence
37	20	100.0	20	6	AR392168	Sequence
38	20	100.0	20	6	AR432430	Sequence
39	20	100.0	20	6	AX023425	Sequence
40	20	100.0	20	6	AX040172	Sequence
41	20	100.0	20	6	AX104566	Sequence
42	20	100.0	20	6	AX104614	Sequence
43	20	100.0	20	6	AX104673	Sequence
44	20	100.0	20	6	AX105185	Sequence
45	20	100.0	20	6	AX135638	Sequence

ALIGNMENTS

RESULT 1
LOCUS A89782 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 4 from Patent WO9832462.
ACCESSION A89782
VERSION A89782.1 GI:6738296
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 4 30-JUL-1998;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES
source location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TCCATGACGTTCCCTGATGCT 20
|||||
Db 1 TCCATGACGTTCCCTGATGCT 20

RESULT 2
LOCUS A89783 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9832462.
ACCESSION A89783
VERSION A89783.1 GI:6738297
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

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OM nucleic - nucleic search, using sw model.

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: Geneseq_1980s:*
- 2: Geneseq_1990s:*
- 3: Geneseq_2000s:*
- 4: Geneseq_2001as:*
- 5: Geneseq_2001bs:*
- 6: Geneseq_2002as:*
- 7: Geneseq_2002bs:*
- 8: Geneseq_2003as:*
- 9: Geneseq_2003bs:*
- 10: Geneseq_2003cs:*
- 11: Geneseq_2003ds:*
- 12: Geneseq_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	AAT88792 Synthetic
2	20	100.0	20	2	Aav45996 Immune ad
3	20	100.0	20	2	Aav45995 Immune ad
4	20	100.0	20	2	Aav27708 Immunosti
5	20	100.0	20	2	Aav27700 Immunosti
6	20	100.0	20	2	Aav27651 Immunosti
7	20	100.0	20	2	Aav72500 Cpg motif
8	20	100.0	20	2	Aaz41879 IL-12 sec
9	20	100.0	20	2	Aaz28190 Chlamydia
10	20	100.0	20	3	Aaa71935 Murine Th
11	20	100.0	20	3	Aaa48598 Immunosti
12	20	100.0	20	3	Aaz60951 Nucleotid
13	20	100.0	20	3	Aaz47955 Immune re
14	20	100.0	20	3	Aaz47826 Immunosti
15	20	100.0	20	3	Aaa90453 Cpg adjuv
16	20	100.0	20	3	Aaz99648 Nucleotid
17	20	100.0	20	3	Aaz99173 Inflammat
18	20	100.0	20	3	Aaz48858 B-cell st
19	20	100.0	20	3	Aaz47621 Parasitic
20	20	100.0	20	3	Aac60281 Immunosti
21	20	100.0	20	4	Aah20398 Cpg motif

22	20	100.0	20	4	Aah43344	Immunomod
23	20	100.0	20	4	Aah50577	Mouse B c
24	20	100.0	20	4	Aah23751	Synthetic
25	20	100.0	20	4	Aah75852	Inflorosp
26	20	100.0	20	4	Aah19285	Cpg Oligo
27	20	100.0	20	4	Aah19294	Cpg Oligo
28	20	100.0	20	4	Aah19304	Cpg Oligo
29	20	100.0	20	4	Aah19257	Phosphoro
30	20	100.0	20	4	Aaf98806	Cpg Immun
31	20	100.0	20	4	Aad02985	Immunomod
32	20	100.0	20	4	Aaf99604	Immunosti
33	20	100.0	20	4	Aaf99558	Immunosti
34	20	100.0	20	4	Aaf99660	Immunosti
35	20	100.0	20	4	Aah20438	Cpg motif
36	20	100.0	20	4	Aaa92365	CG motif
37	20	100.0	20	4	Aah43897	Human hep
38	20	100.0	20	4	ABL35203	Immunosti
39	20	100.0	20	6	ABL35120	Immunosti
40	20	100.0	20	6	ABL35184	Immunosti
41	20	100.0	20	6	ABL35269	Immunosti
42	20	100.0	20	6	ABL35500	Immunosti
43	20	100.0	20	6	ABL35226	Immunosti
44	20	100.0	20	6	ABL35483	Immunosti
45	20	100.0	20	6	ABL35250	Immunosti

ALIGNMENTS

RESULT 1

AAT88792
ID AAT88792 standard; DNA; 20 BP.

AC AAT88792;

DT 24-APR-1998 (first entry)

DE Synthetic phosphorothioate oligonucleotide used as an adjuvant.

XX Parvovirus; feline; canine; T cell epitope; VP1; VP2; vaccine; immunogen;
KW phosphorothioate; cat; dog; mink; adjuvant; ss.

OS Synthetic.

PN WO9740163-A1.

PD 30-OCT-1997.

PF 18-APR-1997; 97WO-EP001943.

PR 19-APR-1996; 96EP-00106217.

XX (COLP/) COLPAN M.

XX Colpan M, Schorr J, Baker HJ, Smith BF;

XX WPI; 1997-535847/49.

XX Vaccine containing nucleic acid expressing parvoviral epitope -
PT particularly both B and T cell epitope(s), for immunisation of cats, dogs
PT and mink against parvoviruses, also as a carrier for other antigens.

PS Claim 17; Page 23; 30pp; English.

XX This is a synthetic phosphorothioate oligonucleotide used as an adjuvant
CC in an anti-parvovirus vaccine. This adjuvant is particularly a DNA,
CC containing unethylylated Cpg motifs i.e. ISO. The ISO contains
CC phosphorothioate linkages and is also a powerful immune activator. The
CC anti-parvovirus vaccine contains nucleic acid encoding at least one
CC parvovirus-specific VP1 or VP2 T/B cell antigenic epitope plus a carrier.
CC The anti-parvovirus vaccine is especially used to protect cats, dogs and
CC mink, e.g. against feline panleukopenia virus, mink enteritis virus or
CC gastroenteritis caused by canine parvovirus (CPV). The vaccine may also

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	20	100.0	20	2	US-09-133-774-11
2	20	100.0	20	3	US-08-386-063-25
3	20	100.0	20	3	US-09-303-862-11
4	20	100.0	20	3	US-08-386-063-25
5	20	100.0	20	3	US-08-738-652-7
6	20	100.0	20	3	US-08-738-652-35
7	20	100.0	20	3	US-08-738-652-44
8	20	100.0	20	3	US-08-738-652-54
9	20	100.0	20	3	US-09-286-098-24
10	20	100.0	20	3	US-08-960-774-7
11	20	100.0	20	3	US-09-082-649B-68
12	20	100.0	20	3	US-09-082-649B-79
13	20	100.0	20	4	US-09-325-193A-19
14	20	100.0	20	4	US-09-191-170-24
15	20	100.0	20	4	US-09-171-425-5
16	20	100.0	20	4	US-09-171-425-14
17	20	100.0	20	4	US-09-690-921-5
18	20	100.0	20	4	US-09-791-500-7
19	20	100.0	20	4	US-09-337-619-7
20	20	100.0	29	4	US-08-848-229-2
21	20	100.0	29	4	US-09-022-965-2
22	18.4	92.0	20	3	US-08-738-652-3
23	18.4	92.0	20	3	US-08-738-652-9
24	18.4	92.0	20	3	US-08-738-652-40
25	18.4	92.0	20	3	US-08-738-652-43
26	18.4	92.0	20	3	US-08-738-652-45
27	18.4	92.0	20	3	US-08-738-652-46

28	18.4	92.0	20	3	US-08-738-652-53
29	18.4	92.0	20	3	US-09-030-701-5
30	18.4	92.0	20	3	US-09-286-098-45
31	18.4	92.0	20	3	US-09-286-098-48
32	18.4	92.0	20	3	US-09-286-098-49
33	18.4	92.0	20	3	US-09-286-098-50
34	18.4	92.0	20	3	US-09-286-098-56
35	18.4	92.0	20	3	US-09-286-098-57
36	18.4	92.0	20	3	US-08-960-774-3
37	18.4	92.0	20	3	US-08-960-774-9
38	18.4	92.0	20	3	US-08-960-774-35
39	18.4	92.0	20	3	US-08-960-774-38
40	18.4	92.0	20	3	US-08-960-774-39
41	18.4	92.0	20	3	US-08-960-774-87
42	18.4	92.0	20	3	US-08-960-774-89
43	18.4	92.0	20	3	US-09-082-649B-71
44	18.4	92.0	20	4	US-09-325-193A-38
45	18.4	92.0	20	4	US-09-325-193A-42

ALIGNMENTS

RESULT 1

US-09-133-774-11
; Sequence 11, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-11

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

US-08-386-063-25
; Sequence 25, Application US/08386063
; Patent No. 6008200
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	20	100.0	20	9	US-09-791-500-7	Sequence 7, Appli
2	20	100.0	20	9	US-09-824-468-24	Sequence 24, Appl
3	20	100.0	20	9	US-09-800-266A-19	Sequence 19, Appl
4	20	100.0	20	9	US-09-846-091-4	Sequence 4, Appli
5	20	100.0	20	9	US-09-895-007A-19	Sequence 19, Appl
6	20	100.0	20	9	US-09-920-313-19	Sequence 19, Appl
7	20	100.0	20	10	US-09-415-142-25	Sequence 25, Appl
8	20	100.0	20	10	US-09-888-326-127	Sequence 127, App
9	20	100.0	20	10	US-09-888-326-566	Sequence 566, App
10	20	100.0	20	10	US-09-888-326-567	Sequence 567, App
11	20	100.0	20	10	US-09-818-918-7	Sequence 7, Appli
12	20	100.0	20	10	US-09-818-918-35	Sequence 35, Appl

13	20	100.0	20	10	US-09-818-918-44	Sequence 44, Appl
14	20	100.0	20	10	US-09-818-918-54	Sequence 54, Appl
15	20	100.0	20	10	US-09-931-583-25	Sequence 25, Appl
16	20	100.0	20	10	US-09-931-583-48	Sequence 48, Appl
17	20	100.0	20	10	US-09-776-479-758	Sequence 758, App
18	20	100.0	20	10	US-09-776-479-806	Sequence 806, App
19	20	100.0	20	10	US-09-776-479-865	Sequence 865, App
20	20	100.0	20	10	US-09-954-987B-84	Sequence 84, Appl
21	20	100.0	20	10	US-09-954-987B-207	Sequence 207, App
22	20	100.0	20	10	US-09-967-464-7	Sequence 7, Appli
23	20	100.0	20	11	US-09-874-991C-27	Sequence 27, Appl
24	20	100.0	20	11	US-09-874-991C-93	Sequence 93, Appl
25	20	100.0	20	11	US-09-874-991C-114	Sequence 114, App
26	20	100.0	20	11	US-09-874-991C-138	Sequence 138, App
27	20	100.0	20	11	US-09-874-991C-165	Sequence 165, App
28	20	100.0	20	11	US-09-874-991C-186	Sequence 186, App
29	20	100.0	20	11	US-09-874-991C-406	Sequence 406, App
30	20	100.0	20	11	US-09-874-991C-425	Sequence 425, App
31	20	100.0	20	11	US-09-776-479-758	Sequence 758, App
32	20	100.0	20	11	US-09-776-479-806	Sequence 806, App
33	20	100.0	20	11	US-09-776-479-865	Sequence 865, App
34	20	100.0	20	11	US-09-965-101-68	Sequence 68, Appl
35	20	100.0	20	11	US-09-965-101-79	Sequence 79, Appl
36	20	100.0	20	13	US-10-023-909A-19	Sequence 19, Appl
37	20	100.0	20	13	US-10-205-150-7	Sequence 7, Appli
38	20	100.0	20	14	US-10-011-635A-1	Sequence 1, Appli
39	20	100.0	20	14	US-10-112-653-10	Sequence 10, Appl
40	20	100.0	20	14	US-10-112-653-11	Sequence 11, Appl
41	20	100.0	20	14	US-10-112-653-731	Sequence 731, App
42	20	100.0	20	14	US-10-112-653-779	Sequence 779, App
43	20	100.0	20	14	US-10-112-653-836	Sequence 836, App
44	20	100.0	20	14	US-10-017-995-758	Sequence 758, App
45	20	100.0	20	14	US-10-017-995-806	Sequence 806, App

ALIGNMENTS

RESULT 1

US-09-791-500-7
; Sequence 7, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Rachmielewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-7

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGATGCT 20

Db 1 TCCATGACGTTCTCTGATGCT 20

RESULT 2

US-09-824-468-24
; Sequence 24, Application US/09824468
; Patent No. US20020064515A1

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:**

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	287	2	BF713668 ESTPBL223
2	18.4	92.0	758	8	CC110844 NDL.76114
3	18.4	92.0	777	6	CB313548 AGENCOURT
4	18.4	92.0	809	6	CB567435 AGENCOURT
5	17.4	87.0	370	5	BY153791 BY153791
6	17.4	87.0	392	1	AI077366 OY87611.x
7	17.4	87.0	408	1	AI086210 OY87611.x
8	17.4	87.0	593	8	CC317873 TAM32-3K8
9	17.4	87.0	688	8	AZ364551 IM0110C22
10	17.4	87.0	882	6	CA493454 AGENCOURT
11	17.4	85.0	389	9	CG260054 AG2CK84TV
12	17.4	85.0	497	9	CL179555 104.388.1
13	17.4	85.0	546	2	AW065908 687002G08
14	17.4	85.0	557	6	CA158051 SCEZR2305
15	17.4	85.0	614	6	CA113844 SCGLB103
16	17.4	85.0	646	6	CA109803 SCUTHR106
17	17.4	85.0	663	6	CA153904 SCVPR2203
18	17.4	85.0	668	6	CA264770 SCAGT304
19	17.4	85.0	683	6	CA182313 SCBGT311
20	17.4	85.0	794	9	CG334934 OGWFR04TH
21	17.4	85.0	842	9	CG319646 OG0A234TV
22	17.4	85.0	864	9	CG318330 OGXB66TH
23	17.4	85.0	915	9	CG318342 OGXB66TH
24	17.4	85.0	1051	6	CF258131 74 Tricho

C 25	16.8	84.0	70	1	AA855652	AA855652 VW70G01.r
C 26	16.8	84.0	97	1	AA082589	AA082589 RN23G09.r
C 27	16.8	84.0	127	8	CC200395	CC200395 ZR0901.Ba
C 28	16.8	84.0	170	7	CN699738	CN699738 E0425G03-
C 29	16.8	84.0	185	5	BY012830	BY012830 BY012830
C 30	16.8	84.0	203	2	BB600029	BB600029 BB600029
C 31	16.8	84.0	216	2	BB590993	BB590993 BB590993
C 32	16.8	84.0	217	9	CL808914	CL808914 OR_CBA002
C 33	16.8	84.0	227	2	BB597403	BB597403 BB597403
C 34	16.8	84.0	242	2	BB604665	BB604665 BB604665
C 35	16.8	84.0	243	2	BB599612	BB599612 BB599612
C 36	16.8	84.0	245	2	BB603788	BB603788 BB603788
C 37	16.8	84.0	255	5	BY059591	BY059591 BY059591
C 38	16.8	84.0	266	2	BB596258	BB596258 BB596258
C 39	16.8	84.0	271	2	BB570188	BB570188 BB570188
C 40	16.8	84.0	272	2	BF913557	BF913557 MR3-UT012
C 41	16.8	84.0	275	2	BB585846	BB585846 BB585846
C 42	16.8	84.0	276	2	BB562448	BB562448 BB562448
C 43	16.8	84.0	277	2	BB601536	BB601536 BB601536
C 44	16.8	84.0	296	2	BB601186	BB601186 BB601186
C 45	16.8	84.0	296	5	BY126554	BY126554 BY126554

ALIGNMENTS

RESULT 1
BF713668

LOCUS

DEFINITION

ESTPBL223 differential display RT-PCR clones Sus scrofa cDNA clone

BL223, mRNA sequence.

ACCESSION

BF713668

VERSION

BF713668.1 GI:18002858

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

1 (bases 1 to 287)

AUTHORS

Ponsuksilli, S., Wimmers, K. and Schellander, K.

TITLE

Identification of porcine liver ESTs by differential display RT-PCR

JOURNAL

Unpublished (2001)

COMMENT

Contact: Ponsuksilli S

Institute of Animal Breeding Science

University of Bonn

Endenicher Allee 15, Bonn 53115, Germany

Seq primer: T7 SP6

High quality sequence stop: 287

POLYA=No.

FEATURES

Location/Qualifiers

1..287

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="BL223"

/note="Organ: liver; cDNA fragments obtained from differential display RT-PCR banding patterns were cloned into pGEM"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 287;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCCGTGCT 20

DB 14 TCCATGACGTTCCGTGCT 33

RESULT 2

CC110844/c

LOCUS

CC110844

758 bp DNA linear GSS 16-APR-2003

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-10
Perfect score: 20
Sequence: 1 tccatgacgttctctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_brg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_ey.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	6 AR078395	Sequence
2	20	100.0	20	6 AR140451	Sequence
3	20	100.0	20	6 AR146388	Sequence
4	20	100.0	20	6 AR146393	Sequence
5	20	100.0	20	6 AR154681	Sequence
6	20	100.0	20	6 BD190417	Microemul
7	20	100.0	20	6 BD205610	Method of
8	20	100.0	20	6 BD205615	Method of
9	20	100.0	20	6 BD222610	Compositi
10	20	100.0	20	6 BD251265	Enhanceme
11	20	100.0	20	6 BD261152	Methods a
12	20	100.0	20	6 BD261157	Methods a
13	20	100.0	20	6 BD261307	Methods a
14	20	100.0	20	6 BD261311	Methods a
15	20	100.0	20	6 BD261560	Vaccine. f
16	20	100.0	20	6 BD267913	Methods f
17	20	100.0	20	6 BD270813	Stereoiso
18	20	100.0	20	6 BD270817	Stereoiso
19	20	100.0	20	6 CQ753470	Sequence

20	100.0	20	6	CQ753471	Sequence
21	20	100.0	20	6 CQ769069	Sequence
22	20	100.0	20	6 CQ774838	Sequence
23	20	100.0	20	6 CQ788113	Sequence
24	20	100.0	20	6 CQ788199	Sequence
25	20	100.0	20	6 CQ815135	Sequence
26	20	100.0	20	6 CQ829537	Sequence
27	20	100.0	20	6 CQ829540	Sequence
28	20	100.0	20	6 AR182879	Sequence
29	20	100.0	20	6 AR182884	Sequence
30	20	100.0	20	6 AR182886	Sequence
31	20	100.0	20	6 AR213886	Sequence
32	20	100.0	20	6 AR213888	Sequence
33	20	100.0	20	6 AR222263	Sequence
34	20	100.0	20	6 AR303118	Sequence
35	20	100.0	20	6 AR309879	Sequence
36	20	100.0	20	6 AR316578	Sequence
37	20	100.0	20	6 AR432433	Sequence
38	20	100.0	20	6 AX015197	Sequence
39	20	100.0	20	6 AX020947	Sequence
40	20	100.0	20	6 AX020953	Sequence
41	20	100.0	20	6 AX040168	Sequence
42	20	100.0	20	6 AX040402	Sequence
43	20	100.0	20	6 AX046992	Sequence
44	20	100.0	20	6 AX063575	Sequence
45	20	100.0	20	6 AX063580	Sequence

ALIGNMENTS

RESULT 1
AR078395
LOCUS AR078395
DEFINITION Sequence 12 from patent US 5962636.
ACCESSION AR078395
VERSION AR078395.1 GI:10005141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bachmaier, K., Hessel, A. John., Neu, N. and Penninger, J. Martin.
TITLE Peptides capable of modulating inflammatory heart disease
JOURNAL Patent: US 5962636-A 12 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2
AR140451
LOCUS AR140451
DEFINITION Sequence 10 from patent US 6207646.
ACCESSION AR140451
VERSION AR140451.1 GI:14482947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.
TITLE Immunostimulatory nucleic acid molecules

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgtctctgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2 AAV60950	Unmethy
2	20	100.0	20	2 AAV7683	Unmethy
3	20	100.0	20	2 AAV7667	Immunost
4	20	100.0	20	2 AAZ41946	IL-12 sec
5	20	100.0	20	2 AAZ41949	IL-12 sec
6	20	100.0	20	2 AAX78802	HPV fusio
7	20	100.0	20	2 AAZ31943	CpG adjuv
8	20	100.0	20	2 AAV74237	CpG-N mot
9	20	100.0	20	2 AAV74244	CpG-N mot
10	20	100.0	20	2 AAV74242	CpG-N mot
11	20	100.0	20	2 AAX88536	Cytosine-
12	20	100.0	20	2 AAZ28191	Chlamydia
13	20	100.0	20	3 AAZ61012	Nucleotid
14	20	100.0	20	3 AAZ61010	Nucleotid
15	20	100.0	20	3 AAZ48025	Immune re
16	20	100.0	20	3 AAZ48022	Immune re
17	20	100.0	20	3 AAZ47885	Immunost
18	20	100.0	20	3 AAZ47887	Immunost
19	20	100.0	20	3 AAZ90447	CpG adjuv
20	20	100.0	20	3 AAZ99174	Inflammat
21	20	100.0	20	3 AAZ99004	CpG motif

22	20	100.0	20	3 AAZ47601	Murine im
23	20	100.0	20	3 AAC60277	Immunost
24	20	100.0	20	3 AAC64136	Immunost
25	20	100.0	20	4 AAH20390	CpG motif
26	20	100.0	20	4 AAH20392	CpG motif
27	20	100.0	20	4 AAH50580	CpG motif
28	20	100.0	20	4 AAH19260	CpG oligo
29	20	100.0	20	4 AAF98805	CpG immun
30	20	100.0	20	4 AAF59506	Immunost
31	20	100.0	20	4 AAF59501	Immunost
32	20	100.0	20	4 AAC82106	Oligonuct
33	20	100.0	20	4 AAF99748	Immunost
34	20	100.0	20	4 AAF99745	Immunost
35	20	100.0	20	4 AAF98944	Immunost
36	20	100.0	20	4 AAF99752	Immunost
37	20	100.0	20	4 AAF99175	Immunost
38	20	100.0	20	4 AAF99750	Immunost
39	20	100.0	20	4 AAF99744	Immunost
40	20	100.0	20	4 AAF99751	Immunost
41	20	100.0	20	4 AAF99012	Immunost
42	20	100.0	20	4 AAF99746	Immunost
43	20	100.0	20	4 AAF99753	Immunost
44	20	100.0	20	4 AAF99817	Immunost
45	20	100.0	20	4 AAF99749	Immunost

ALIGNMENTS

RESULT 1
AAV60950
ID AAV60950 standard; DNA; 20 BP.
XX
AC AAV60950;
XX
DT 14-DEC-1998 (first entry)
XX
DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
KW ss; unmethylated CpG dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.
OS Synthetic.
XX
PN WO9840100-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US004703.
XX
PR 10-MAR-1997; 97US-0040376P.
XX
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PI (IOWA) UNIV IOWA RES FOUND.
XX
PI Davis HL, Schorr J, Krieg AM;
XX
DR WPI; 1998-520792/44.
XX
PT Use of oligonucleotides containing an unmethylated CpG dinucleotide -
PT useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
PT for inducing immune response in subject.
XX
PS Claim 14; Page 35; 67pp; English.
XX
CC Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
CC affect the immune response in a subject by activating natural killer
CC cells or redirecting a subject's immune response from a Th2 to a Th1
CC response by inducing monocytic and other cells to produce Th1 cytokines.
CC These nucleic acids containing at least 1 unmethylated CpG can be used as
CC an adjuvant, specifically to induce an immune response against an
CC antigenic protein, and are used particularly for virally mediated

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgttcttcgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
5: /cgn2_6/prodata/1/ina/PTUS COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfileseq.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-09-133-774-12
2	20	100.0	20	3	US-09-303-862-12
3	20	100.0	20	3	US-08-738-652-10
4	20	100.0	20	3	US-09-030-701-62
5	20	100.0	20	3	US-09-286-098-100
6	20	100.0	20	3	US-09-286-098-105
7	20	100.0	20	3	US-08-960-774-10
8	20	100.0	20	3	US-09-082-649B-51
9	20	100.0	20	3	US-09-082-649B-56
10	20	100.0	20	3	US-09-082-649B-58
11	20	100.0	20	4	US-09-325-193A-86
12	20	100.0	20	4	US-09-325-193A-90
13	20	100.0	20	4	US-09-191-170-97
14	20	100.0	20	4	US-09-690-921-1
15	20	100.0	20	4	US-09-301-829A-1
16	20	100.0	20	4	US-09-692-170C-42
17	20	100.0	20	4	US-09-337-619-10
18	20	100.0	20	4	US-10-405-231A-42
19	20	100.0	20	4	US-10-238-607-42
20	20	100.0	20	4	US-09-984-365-42
21	20	100.0	20	4	US-09-565-906-1
22	20	100.0	20	4	US-09-257-188A-2
23	20	100.0	44	3	US-09-082-649B-12
24	20	100.0	44	3	US-09-082-649B-13
25	17	85.0	17	3	US-09-030-701-39
26	17	85.0	17	3	US-09-286-098-70
27	17	85.0	17	3	US-08-960-774-70

28	17	85.0	17	4	US-09-325-193A-60	Sequence 60, Appl
29	17	85.0	17	4	US-09-191-170-64	Sequence 64, Appl
30	17	85.0	17	4	US-09-337-619-70	Sequence 70, Appl
31	16.8	84.0	20	2	US-09-133-774-11	Sequence 11, Appl
32	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl
33	16.8	84.0	20	3	US-09-303-862-11	Sequence 11, Appl
34	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl
35	16.8	84.0	20	3	US-08-738-652-7	Sequence 7, Appl
36	16.8	84.0	20	3	US-08-738-652-35	Sequence 35, Appl
37	16.8	84.0	20	3	US-08-738-652-44	Sequence 44, Appl
38	16.8	84.0	20	3	US-08-738-652-54	Sequence 54, Appl
39	16.8	84.0	20	3	US-09-030-701-42	Sequence 42, Appl
40	16.8	84.0	20	3	US-09-286-098-74	Sequence 24, Appl
41	16.8	84.0	20	3	US-09-286-098-73	Sequence 73, Appl
42	16.8	84.0	20	3	US-09-286-098-84	Sequence 84, Appl
43	16.8	84.0	20	3	US-08-960-774-7	Sequence 7, Appl
44	16.8	84.0	20	3	US-08-960-774-73	Sequence 73, Appl
45	16.8	84.0	20	3	US-09-082-649B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-133-774-12
; Sequence 12, Application US/09133774B

; Patent No. 5962636

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart

; TITLE OF INVENTION: Disease

; FILE REFERENCE: A-536

; CURRENT APPLICATION NUMBER: US/09/133,774B

; CURRENT FILING DATE: 1998-08-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia trachomatis

; FEATURE:

; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a

; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from

; OTHER INFORMATION: Chlamydia trachomatis.

US-09-133-774-12

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTTCGACGTT 20

|||||

Db 1 TCCATGACGTTCTTCGACGTT 20

RESULT 2

US-09-303-862-12

; Sequence 12, Application US/09303862

; Patent No. 6034230

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Heart

; TITLE OF INVENTION: Disease

; FILE REFERENCE: A-536

; CURRENT APPLICATION NUMBER: US/09/303,862

; CURRENT FILING DATE: 1999-05-03

; EARLIER APPLICATION NUMBER: 09/133,774

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
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15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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3	20	100.0	20	9	US-09-824-468-100
4	20	100.0	20	9	US-09-824-468-105
5	20	100.0	20	9	US-09-949-194-1
6	20	100.0	20	9	US-09-917-222-1
7	20	100.0	20	9	US-09-800-266A-86
8	20	100.0	20	9	US-09-800-266A-90
9	20	100.0	20	9	US-09-895-007A-86
10	20	100.0	20	9	US-09-895-007A-90
11	20	100.0	20	9	US-09-920-313-86
12	20	100.0	20	9	US-09-920-313-90

13	20	100.0	20	10	US-09-888-326-560	Sequence 560, App
14	20	100.0	20	10	US-09-888-326-561	Sequence 561, App
15	20	100.0	20	10	US-09-888-326-562	Sequence 562, App
16	20	100.0	20	10	US-09-888-326-563	Sequence 563, App
17	20	100.0	20	10	US-09-818-918-10	Sequence 10, Appl
18	20	100.0	20	10	US-09-931-583-47	Sequence 69, Appl
19	20	100.0	20	10	US-09-776-479-69	Sequence 47, Appl
20	20	100.0	20	10	US-09-776-479-117	Sequence 137, App
21	20	100.0	20	10	US-09-776-479-152	Sequence 152, App
22	20	100.0	20	10	US-09-776-479-153	Sequence 153, App
23	20	100.0	20	10	US-09-776-479-223	Sequence 223, App
24	20	100.0	20	10	US-09-776-479-302	Sequence 302, App
25	20	100.0	20	10	US-09-776-479-948	Sequence 948, App
26	20	100.0	20	10	US-09-776-479-949	Sequence 949, App
27	20	100.0	20	10	US-09-776-479-950	Sequence 950, App
28	20	100.0	20	10	US-09-776-479-951	Sequence 951, App
29	20	100.0	20	10	US-09-776-479-952	Sequence 952, App
30	20	100.0	20	10	US-09-776-479-953	Sequence 953, App
31	20	100.0	20	10	US-09-776-479-954	Sequence 954, App
32	20	100.0	20	10	US-09-776-479-955	Sequence 955, App
33	20	100.0	20	10	US-09-776-479-956	Sequence 956, App
34	20	100.0	20	10	US-09-776-479-957	Sequence 957, App
35	20	100.0	20	10	US-09-776-479-958	Sequence 958, App
36	20	100.0	20	10	US-09-776-479-1023	Sequence 1023, App
37	20	100.0	20	10	US-09-954-987B-83	Sequence 83, Appl
38	20	100.0	20	10	US-09-967-464-1	Sequence 1, Appl
39	20	100.0	20	10	US-09-984-365-42	Sequence 42, Appl
40	20	100.0	20	11	US-09-776-479-69	Sequence 69, Appl
41	20	100.0	20	11	US-09-776-479-137	Sequence 137, App
42	20	100.0	20	11	US-09-776-479-152	Sequence 152, App
43	20	100.0	20	11	US-09-776-479-153	Sequence 153, App
44	20	100.0	20	11	US-09-776-479-223	Sequence 223, App
45	20	100.0	20	11	US-09-776-479-302	Sequence 302, App

ALIGNMENTS

RESULT 1
US-09-760-506-3
; Sequence 3, Application US/09760506
; Publication No. US20010034330A1
; GENERAL INFORMATION:
; APPLICANT: Kensil, Charlotte
; TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of CpG and
; FILE REFERENCE: 8449-153-999
; CURRENT APPLICATION NUMBER: US/09/760,506
; CURRENT FILING DATE: 2002-01-12
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/200,853
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/175,840
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/128,608
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/095,913
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-09-760-506-3

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCCTGACGTT 20
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgttcttcgacgtt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2.*
- 3: gb_hcc.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	16.8	84.0	287	2	BF713668	BF713668 ESTPBL223
5	16.8	84.0	389	9	CG260054	CG260054 OG2CK94TV
6	16.8	84.0	464	1	AA171941	AA171941 ZP24f01.s
7	16.8	84.0	497	9	CL179555	CL179555 104.388.1
8	16.8	84.0	516	2	BF156008	BF156008 RC0-H7095
9	16.8	84.0	546	2	AW065908	AW065908 687002G08
10	16.8	84.0	557	6	CA158051	CA158051 SCEZR2305
11	16.8	84.0	614	6	CA113844	CA113844 SCGLR103
12	16.8	84.0	646	6	CA109803	CA109803 SCUTR106
13	16.8	84.0	663	6	CA153904	CA153904 SCVPR2203
14	16.8	84.0	669	6	CA264770	CA264770 SCAGR304
15	16.8	84.0	683	6	CA182313	CA182313 SCBGS7311
16	16.8	84.0	715	5	BU253412	BU253412 603415072
17	16.8	84.0	758	8	CC110844	CC110844 NDL.76114
18	16.8	84.0	794	9	CG334934	CG334934 OGFPR04TH
19	16.8	84.0	797	9	CNS02N06	AL205647 Tetraodon
20	16.8	84.0	814	5	BU205165	BU205165 603951055
21	16.8	84.0	821	9	CNS03G84	AL242653 Tetraodon
22	16.8	84.0	842	9	CG319646	CG319646 OGA234TV
23	16.8	84.0	864	9	CG318330	CG318330 OGXB66TV
24	16.8	84.0	908	6	CD791886	CD791886 EST663247

25	16.8	84.0	915	9	CG318342	CG318342 OGXB66TV
26	16.8	84.0	958	5	BQ82047	BQ82047 AGENCOURT
c	27	16.8	992	5	CNS04004	AL262221 Tetraodon
28	16.8	84.0	994	9	CNS0421L	AL271542 Tetraodon
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c	31	16.4	318	8	AZ578302	AZ578302 21c11 Sho
c	32	16.4	392	6	BY630307	BY630307 BY630307
c	33	16.4	398	4	BI033356	BI033356 PM2-NN008
c	34	16.4	553	2	BB767360	BB767360 BB767360
c	35	16.4	596	4	BM592203	BM592203 170006685
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c	38	16.4	665	2	BB183341	BB183341 BB183341
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c	40	16.4	695	7	CF531954	CF531954 UI-M-FY0-
c	41	16.4	712	4	BG067865	BG067865 H3059A10-
c	42	16.4	733	7	CF537365	CF537365 UI-M-G10-
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44	16.4	82.0	824	9	CNS01XP2	AL172016 Tetraodon
45	16.4	82.0	880	6	CD778747	CD778747 EST650108

ALIGNMENTS

RESULT 1
LOCUS CC709713 886 bp DNA linear GSS 19-JUN-2003
DEFINITION OGUBV23TV ZM 0.7 1.5 KB Zea mays genomic clone ZM85Ma0404D21,
genomic survey sequence.
ACCESSION CC709713 GI:32114489
VERSION CC709713.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
ciade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 886)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OGUBV23TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM85Ma0404D21"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 92.0%; Score 18.4; DB 9; Length 886;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCATGACGTTCTTCGACGTT 20
|||||
DB 31 TCCATGACGTTCCGACGTT 50

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 999gtcaacgttgagg999g 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	20	6	ARI154761 Sequence
3	20	100.0	20	6	BD190419 Microemul
4	20	100.0	20	6	BD251267 Enhanceme
5	20	100.0	20	6	ARI182880 Sequence
6	20	100.0	20	6	ARI182887 Sequence
7	20	100.0	20	6	AR222213 Sequence
8	20	100.0	20	6	AR432435 Sequence
9	20	100.0	20	6	AX063578 Sequence
10	20	100.0	20	6	AX088932 Sequence
11	20	100.0	20	6	AX104327 Sequence
12	20	100.0	20	6	AX104575 Sequence
13	20	100.0	20	6	AX104776 Sequence
14	20	100.0	20	6	AX104777 Sequence
15	20	100.0	20	6	AX105103 Sequence
16	20	100.0	20	6	AX105236 Sequence
17	20	100.0	20	6	AX135634 Sequence
18	20	100.0	20	6	AX194489 Sequence
19	20	100.0	20	6	AX355408 Sequence

20	20	100.0	20	6	AX355409	Sequence
21	20	100.0	20	6	AX465439	Sequence
22	20	100.0	20	6	AX468483	Sequence
23	20	100.0	20	6	AX547380	Sequence
24	20	100.0	20	6	AX547628	Sequence
25	20	100.0	20	6	AX547829	Sequence
26	20	100.0	20	6	AX547830	Sequence
27	20	100.0	20	6	BD009060	Immunosti
28	20	100.0	20	6	BD069974	Use of nu
29	20	100.0	21	6	AX104812	Sequence
30	20	100.0	21	6	AX105257	Sequence
31	20	100.0	21	6	AX547865	Sequence
32	20	100.0	24	6	AX104326	Sequence
33	20	100.0	24	6	AX547379	Sequence
34	19	95.0	19	6	CQ753472	Sequence
35	19	95.0	19	6	CQ753473	Sequence
36	19	95.0	19	6	AX194446	Sequence
37	19	95.0	19	6	AX465396	Sequence
38	19	95.0	19	6	AX771751	Sequence
39	19	95.0	19	6	AX771752	Sequence
40	18.4	92.0	20	6	AR096686	Sequence
41	18.4	92.0	20	6	ARI35030	Sequence
42	18.4	92.0	20	6	AX342378	Sequence
43	18.4	92.0	20	6	AX342405	Sequence
44	18.4	92.0	20	6	AX342438	Sequence
45	17.4	87.0	19	6	ARI46340	Sequence

ALIGNMENTS

RESULT 1	ARI40453	Sequence 12 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
ARI40453	Sequence 12 from patent US 6207646.					
LOCUS	ARI40453					
DEFINITION	Sequence 12 from patent US 6207646.					
ACCESSION	ARI40453					
VERSION	ARI40453.1	GI:14482949				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 20)					
TITLE	Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.					
JOURNAL	Immunostimulatory nucleic acid molecules					
FEATURES	Patent: US 6207646-A 12 27-MAR-2001;					
source	Location/Qualifiers					
	1..20					
	/organism="unknown"					
	/mol_type="unassigned DNA"					

Query Match	100.0%;	Score 20;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 32;		
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	GGGGTCAACGTTGAGGGGGG	20	
Db	1	GGGGTCAACGTTGAGGGGGG	20	

RESULT 2	ARI154761	Sequence 90 from patent US 6239116.	20 bp	DNA	linear	PAT 08-AUG-2001
ARI154761	Sequence 90 from patent US 6239116.					
LOCUS	ARI154761					
DEFINITION	Sequence 90 from patent US 6239116.					
ACCESSION	ARI154761					
VERSION	ARI154761.1	GI:15122814				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 20)					
TITLE	Krieg, A.M. and Kline, J.N.					
	Immunostimulatory nucleic acid molecules					

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	2 AAT16894	Aat16894 Immunomod
2	20	100.0	20	2 AAV47684	Aav47684 Unmethyla
3	20	100.0	20	2 AAV27654	Aav27654 Immunosti
4	20	100.0	20	2 AAV74238	Aav74238 CpG-N mot
5	20	100.0	20	2 AAV74245	Aav74245 CpG-N mot
6	20	100.0	20	3 AAG90449	Aag90449 CpG adjuv
7	20	100.0	20	4 AAH20394	Aah20394 CpG motif
8	20	100.0	20	4 AAH50658	Aah50658 Immune re
9	20	100.0	20	4 AAH19262	Aah19262 Oligonuc
10	20	100.0	20	4 AAF98854	Aaf98854 Poly-G im
11	20	100.0	20	4 AAF98731	Aaf98731 Human IFN
12	20	100.0	20	4 AAC80669	Aac80669 Immunogen
13	20	100.0	20	4 AAF59504	Aaf59504 Immunosti
14	20	100.0	20	4 AAF99567	Aaf99567 Immunosti
15	20	100.0	20	4 AAF99764	Aaf99764 Immunosti
16	20	100.0	20	4 AAF99390	Aaf99390 Immunosti
17	20	100.0	20	4 AAF99763	Aaf99763 Immunosti
18	20	100.0	20	4 AA92361	Aa92361 CG motif
19	20	100.0	20	4 AAS09639	Aas09639 Immunorea
20	20	100.0	20	5 AAF27750	Aaf27750 P. falcip
21	20	100.0	20	6 ABS78484	Ab878484 Angiogene

22	20	100.0	20	6 ABS78485	Ab878485 Angiogene
23	20	100.0	20	6 ABS78283	Ab878283 Angiogene
24	20	100.0	20	6 ABS78035	Ab878035 Angiogene
25	20	100.0	20	6 ABL39032	Ab139032 Immunosti
26	20	100.0	20	6 ABL39033	Ab139033 Immunosti
27	20	100.0	20	6 ABK46517	Abk46517 Immunosti
28	20	100.0	20	6 AAL44488	Aal44488 CpG motif
29	20	100.0	20	6 ABS70558	Ab870558 Dendritic
30	20	100.0	20	8 ACC48308	Acc48308 CpG oligo
31	20	100.0	20	8 ABZ80163	Abz80163 Immunosti
32	20	100.0	20	9 ACC83113	Acc83113 D class C
33	20	100.0	20	9 ACD99810	Acd99810 Immunosti
34	20	100.0	20	9 ACH03105	Ach03105 Immunosti
35	20	100.0	20	9 ACH03288	Ach03288 Immunosti
36	20	100.0	20	9 ADB37069	Adb37069 Immunosti
37	20	100.0	20	9 ADB37266	Adb37266 Immunosti
38	20	100.0	20	9 ADB36892	Adb36892 Immunosti
39	20	100.0	20	9 ADB37265	Adb37265 Immunosti
40	20	100.0	20	10 AAD60208	Aad60208 Oligonuc
41	20	100.0	20	10 ADG68114	Adg68114 Unmethyla
42	20	100.0	20	12 ADI01054	Adi01054 Immunosti
43	20	100.0	20	12 ACA63219	Ac63219 Toll-like
44	20	100.0	20	12 ADM99023	Adm99023 Immunosti
45	20	100.0	20	12 ADO04739	Ado04739 CpG oligo

ALIGNMENTS

RESULT 1

AAT16894

ID AAT16894 standard; DNA; 20 BP.

XX

AC AAT16894;

XX

DT 06-SEP-1996 (first entry)

XX

DE Immunomodulatory oligonucleotide contg. unmethylated C-G dinucleotide.

XX

KW Unmethylated; immunomodulator; B cell activation; vaccine;

XX

KW response stimulation; autoimmune disease; infection; ss.

XX

OS Synthetic.

XX

PN WO9602555-A1.

XX

PD 01-FEB-1996.

XX

PF 07-FEB-1995; 95WO-US001570.

XX

PR 15-JUL-1994; 94US-00276358.

XX

PA (IOWA) UNIV IOWA STATE RES FOUND INC.

XX

PI Krieg AM;

XX

DR WPI; 1996-105847/11.

XX

PT Immunomodulatory oligo:nucleotide(s) contg. an un-methylated CpG di-

XX

PT nucleotide - used for stimulating activity or when methylated for

XX

PS inhibitory activity.

XX

PS Claim 5; Page 39; 45pp; English.

XX

CC AAT16894-T16898 are immunomodulatory oligonucleotides contg. at least one

XX

CC unmethylated C-G dinucleotide. The oligonucleotides can be used to

XX

CC activate B cells and natural killer cells. They can be used for treating,

XX

CC preventing or ameliorating an immune system deficiency, e.g. a tumour,

XX

CC cancer or a viral, fungal, bacterial or parasitic infection. They are

XX

SQ also useful in stimulating a subject's response to a vaccine.

SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagg9999 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 3: /cgn2_6/prodata1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-08-738-652-12
2	20	100.0	20	3	US-09-030-701-63
3	20	100.0	20	3	US-08-960-774-90
4	20	100.0	20	3	US-09-082-649B-52
5	20	100.0	20	3	US-09-082-649B-59
6	20	100.0	20	4	US-09-191-170-47
7	20	100.0	20	4	US-09-337-619-12
8	18.4	92.0	20	3	US-08-386-063-1
9	18.4	92.0	20	3	US-08-386-063-1
10	17.4	87.0	19	3	US-09-030-701-21
11	17.4	87.0	19	3	US-09-286-098-52
12	17.4	87.0	19	3	US-08-960-774-12
13	17.4	87.0	19	4	US-09-325-193A-46
14	16.8	84.0	20	4	US-09-786-532-2
15	16	80.0	1426	4	US-09-464-535-41
16	15.8	79.0	1674	4	US-09-482-273-78
17	15.8	79.0	2312	4	US-09-620-312D-921
18	15.8	79.0	2312	4	US-09-620-312D-921
19	15.2	76.0	20	3	US-08-386-063-27
20	15.2	76.0	20	3	US-08-386-063-27
21	15.2	76.0	379	4	US-09-270-767-2945
22	15.2	76.0	379	4	US-09-270-767-18227
23	15.2	76.0	409	4	US-09-513-999C-15817
24	15.2	76.0	504	4	US-09-470-191-18
25	15.2	76.0	634	1	US-08-451-947-1
26	15.2	76.0	634	2	US-08-424-826A-1
27	15.2	76.0	634	3	US-08-928-694-1

C 28	15.2	76.0	634	4	US-08-450-842-1	Sequence 1, Appli
C 29	15.2	76.0	634	4	US-08-451-390-1	Sequence 1, Appli
C 30	15.2	76.0	634	5	PCT-US91-06950-1	Sequence 1, Appli
C 31	15.2	76.0	813	4	US-09-602-787A-471	Sequence 471, App
C 32	15.2	76.0	831	4	US-09-540-236-799	Sequence 799, App
C 33	15.2	76.0	1404	1	US-07-796-106-22	Sequence 22, Appl
C 34	15.2	76.0	1533	4	US-09-657-013-21	Sequence 21, Appl
C 35	15.2	76.0	1652	4	US-09-657-013-26	Sequence 26, Appl
C 36	15.2	76.0	1669	4	US-09-657-013-20	Sequence 20, Appl
C 37	15.2	76.0	2351	4	US-09-657-013-23	Sequence 23, Appl
C 38	15.2	76.0	3220	2	US-08-225-488-1	Sequence 1, Appli
C 39	15.2	76.0	10091	4	US-09-657-013-24	Sequence 24, Appl
C 40	15.2	76.0	10182	4	US-09-657-013-25	Sequence 25, Appl
C 41	15.2	76.0	10182	4	US-09-657-013-27	Sequence 27, Appl
C 42	15.2	76.0	10182	4	US-09-657-013-28	Sequence 28, Appl
C 43	15.2	76.0	11703	3	US-09-101-886B-3	Sequence 3, Appli
C 44	15.2	76.0	94750	4	US-09-596-002-38	Sequence 38, Appl
C 45	15.2	76.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20
|||
DB 1 GGGGTCAACGTTGAGGGGG 20

RESULT 2

US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 999gtcaacttgag99999 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	10	US-09-888-326-436
2	20	100.0	20	10	US-09-888-326-437
3	20	100.0	20	10	US-09-818-918-12
4	20	100.0	20	10	US-09-776-479-519
5	20	100.0	20	10	US-09-776-479-767
6	20	100.0	20	10	US-09-776-479-968
7	20	100.0	20	10	US-09-776-479-969
8	20	100.0	20	10	US-09-967-464-3
9	20	100.0	20	11	US-09-776-479-519
10	20	100.0	20	11	US-09-776-479-767
11	20	100.0	20	11	US-09-776-479-968
12	20	100.0	20	11	US-09-776-479-969

13	20	100.0	20	11	US-09-965-101-52	Sequence 52, Appl
14	20	100.0	20	11	US-09-965-101-59	Sequence 59, Appl
15	20	100.0	20	14	US-10-112-653-496	Sequence 496, App
16	20	100.0	20	14	US-10-112-653-740	Sequence 740, App
17	20	100.0	20	14	US-10-112-653-923	Sequence 923, App
18	20	100.0	20	14	US-10-017-995-519	Sequence 519, App
19	20	100.0	20	14	US-10-017-995-767	Sequence 767, App
20	20	100.0	20	14	US-10-017-995-968	Sequence 968, App
21	20	100.0	20	14	US-10-017-995-969	Sequence 969, App
22	20	100.0	20	15	US-10-161-229-47	Sequence 47, Appl
23	20	100.0	20	15	US-10-194-035-89	Sequence 89, Appl
24	20	100.0	20	15	US-10-224-523-35	Sequence 35, Appl
25	20	100.0	20	15	US-10-187-264A-12	Sequence 12, Appl
26	20	100.0	20	15	US-10-306-523-12	Sequence 12, Appl
27	20	100.0	20	15	US-10-314-578-519	Sequence 519, App
28	20	100.0	20	15	US-10-314-578-767	Sequence 767, App
29	20	100.0	20	15	US-10-314-578-968	Sequence 968, App
30	20	100.0	20	15	US-10-314-578-969	Sequence 969, App
31	20	100.0	20	16	US-10-455-247-3	Sequence 3, Appl
32	20	100.0	20	17	US-10-719-493-12	Sequence 12, Appl
33	20	100.0	20	17	US-10-627-331-12	Sequence 12, Appl
34	20	100.0	20	17	US-10-743-625-12	Sequence 12, Appl
35	20	100.0	20	17	US-10-769-282-12	Sequence 12, Appl
36	20	100.0	20	18	US-10-817-165-12	Sequence 12, Appl
37	20	100.0	20	18	US-10-877-407-30	Sequence 30, Appl
38	20	100.0	20	18	US-10-831-778-519	Sequence 519, App
39	20	100.0	20	18	US-10-831-778-767	Sequence 767, App
40	20	100.0	20	18	US-10-831-778-968	Sequence 968, App
41	20	100.0	20	18	US-10-831-778-969	Sequence 969, App
42	20	100.0	20	18	US-10-486-755-14	Sequence 14, Appl
43	20	100.0	21	10	US-09-776-479-1004	Sequence 1004, Ap
44	20	100.0	21	11	US-09-776-479-1004	Sequence 1004, Ap
45	20	100.0	21	14	US-10-112-653-957	Sequence 957, App

ALIGNMENTS

RESULT 1
US-09-888-326-436
; Sequence 436, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 436
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-436

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20

DB 1 GGGGTCAACGTTGAGGGGG 20

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
: 274.665 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	87.0	260	2	BB584327
2	17.4	87.0	708	2	BB629098
3	17.4	87.0	737	4	EG747032
4	17.4	87.0	957	5	BU956037
5	17.4	87.0	1244	5	BE962736
6	17	85.0	787	5	BX386891
7	17	85.0	791	9	CC506640
8	17	85.0	1008	5	BX356727
9	16.8	84.0	196	6	CA452850
10	16.8	84.0	244	7	CN657439
11	16.8	84.0	382	5	BY084323
12	16.8	84.0	406	4	BM001652
13	16.8	84.0	414	5	EX678404
14	16.8	84.0	457	5	BY277221
15	16.8	84.0	468	6	CA577271
16	16.8	84.0	473	7	CO076646
17	16.8	84.0	486	7	CF484305
18	16.8	84.0	508	4	BM003672
19	16.8	84.0	516	7	CO076740
20	16.8	84.0	522	7	CK391782
21	16.8	84.0	532	1	AL830714
22	16.8	84.0	533	4	BG355722
23	16.8	84.0	558	5	BX253788
24	16.8	84.0	569	7	CF895871

C 25	16.8	84.0	594	7	CF897160
C 26	16.8	84.0	595	7	CF896689
C 27	16.8	84.0	607	5	BQ18485
C 28	16.8	84.0	669	6	CB663538
C 29	16.8	84.0	680	4	BI716183
C 30	16.8	84.0	690	6	BY758462
C 31	16.8	84.0	692	8	BZ714778
C 32	16.8	84.0	700	2	BF607967
C 33	16.8	84.0	755	8	AZ099791
C 34	16.8	84.0	763	9	CC927270
C 35	16.8	84.0	766	8	BZ714768
C 36	16.8	84.0	777	8	AQ742337
C 37	16.8	84.0	793	8	BZ829333
C 38	16.8	84.0	806	4	BG571384
C 39	16.8	84.0	830	5	BU960761
C 40	16.8	84.0	837	5	BU940725
C 41	16.8	84.0	841	6	CA315476
C 42	16.8	84.0	855	5	BQ887367
C 43	16.8	84.0	873	7	CO809524
C 44	16.8	84.0	876	5	BQ942170
C 45	16.8	84.0	877	6	CB943960

ALIGNMENTS

RESULT 1
BB584327
LOCUS
DEFINITION
BB584327 RIKEN full-length enriched, adult male epididymis Mus
ACCESSION
BB584327
VERSION
BB584327.1 GI:11480871
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 260)
Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodojima,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toyota,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-38
Perfect score: 20
Sequence: 1 tccatgcgttcctgatgct 20

Scoring table: IDENTITY NUC
Gapop 10'0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.:

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2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR140484 Sequence
2	20	100.0	20	6	AR140494 Sequence
3	20	100.0	20	6	AR146336 Sequence
4	20	100.0	20	6	AR146344 Sequence
5	20	100.0	20	6	AR146345 Sequence
6	20	100.0	20	6	AR154709 Sequence
7	20	100.0	20	6	BD190422 Microemul
8	20	100.0	20	6	BD190422 Sequence
9	20	100.0	20	6	BD205558 Method of
10	20	100.0	20	6	BD205566 Method of
11	20	100.0	20	6	BD205567 Method of
12	20	100.0	20	6	BD261100 Enhanceme
13	20	100.0	20	6	BD261108 Methods a
14	20	100.0	20	6	BD261109 Methods a
15	20	100.0	20	6	BD261109 Methods a
16	20	100.0	20	6	BD261270 Methods a
17	20	100.0	20	6	BD267867 Methods a
18	20	100.0	20	6	BD267874 Methods f
19	20	100.0	20	6	BD270776 Stereoiso
					AR182899 Sequence

20	20	100.0	20	6	AR213849 Sequence
21	20	100.0	20	6	AR222209 Sequence
22	20	100.0	20	6	AR222217 Sequence
23	20	100.0	20	6	AR432461 Sequence
24	20	100.0	20	6	AX045773 Sequence
25	20	100.0	20	6	AX045774 Sequence
26	20	100.0	20	6	AX103944 Sequence
27	20	100.0	20	6	AX104567 Sequence
28	20	100.0	20	6	AX135637 Sequence
29	20	100.0	20	6	AX351747 Sequence
30	20	100.0	20	6	AX351813 Sequence
31	20	100.0	20	6	AX351836 Sequence
32	20	100.0	20	6	AX351864 Sequence
33	20	100.0	20	6	AX351885 Sequence
34	20	100.0	20	6	AX351910 Sequence
35	20	100.0	20	6	AX352126 Sequence
36	20	100.0	20	6	AX352145 Sequence
37	20	100.0	20	6	AX355034 Sequence
38	20	100.0	20	6	AX355583 Sequence
39	20	100.0	20	6	AX455619 Sequence
40	20	100.0	20	6	AX465348 Sequence
41	20	100.0	20	6	AX468486 Sequence
42	20	100.0	20	6	AX546997 Sequence
43	20	100.0	20	6	AX547620 Sequence
44	20	100.0	20	6	AX786558 Sequence
45	20	100.0	20	6	BD009091 Immunosti

ALIGNMENTS

RESULT 1	AR140484	Sequence 43 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR140484					
DEFINITION	AR140484					
ACCESSION	AR140484					
VERSION	AR140484.1	GI:14482980				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.					
TITLE	Immunostimulatory nucleic acid molecules					
JOURNAL	Patent: US 6207646-A 43 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
	/organism="unknown"					
	/mol_type="unassigned DNA"					

ORIGIN

Query Match	100.0%	Score 20;	DB 6;	Length 20;
Best Local Similarity	100.0%	Pred. No. 8.7;	0;	Indels 0;
Mismatches	20;	Conservative 0;	Mismatches 0;	Gaps 0;
OY	1	TCCATGTCGTTCTCGATGCT	20	
Db	1	TCCATGTCGTTCTCGATGCT	20	
RESULT 2	AR140494	Sequence 53 from patent US 6207646.	20 bp	DNA
LOCUS	AR140494			
DEFINITION	AR140494			
ACCESSION	AR140494			
VERSION	AR140494.1	GI:14482990		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 20)			
AUTHORS	Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.			
TITLE	Immunostimulatory nucleic acid molecules			

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgcgtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq_23Sep04:*

1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2 AAV60952	Unmethyla
2	20	100.0	20	2 AAV47688	Unmethyla
3	20	100.0	20	2 AAV27647	Immunosti
4	20	100.0	20	2 AAV27707	Immunosti
5	20	100.0	20	2 AAZ41894	IL-12 sec
6	20	100.0	20	2 AAZ41903	IL-12 sec
7	20	100.0	20	3 AAZ60973	Nucleotid
8	20	100.0	20	3 AAZ47979	Immune re
9	20	100.0	20	3 AAZ47978	Immune re
10	20	100.0	20	3 AAZ47970	Immune re
11	20	100.0	20	3 AAZ47848	Immunosti
12	20	100.0	20	3 AAZ90452	CpG adjuv
13	20	100.0	20	3 AAZ47641	Parasitic
14	20	100.0	20	3 AAZ47634	Parasitic
15	20	100.0	20	3 AAZ63585	Immune st
16	20	100.0	20	4 AAZ20397	CpG motif
17	20	100.0	20	4 AAC87224	Immunosti
18	20	100.0	20	4 AAC87225	Methylate
19	20	100.0	20	4 AAH50608	CpG motif
20	20	100.0	20	4 AAH19303	Non CpG o
21	20	100.0	20	4 AAH19293	CpG Oligo

C	22	20	100.0	20	4 AAF99011	Immunosti
	23	20	100.0	20	4 AAF99559	Immunosti
	24	20	100.0	20	4 AAA92364	CG motif
	25	20	100.0	20	6 ABL35498	Immunosti
	26	20	100.0	20	6 ABL35265	Immunosti
	27	20	100.0	20	6 ABL35288	Immunosti
	28	20	100.0	20	6 ABL35199	Immunosti
	29	20	100.0	20	6 ABL35220	Immunosti
	30	20	100.0	20	6 ABL35515	Immunosti
	31	20	100.0	20	6 ABL35135	Immunosti
	32	20	100.0	20	6 ABL35246	Immunosti
C	33	20	100.0	20	6 ABS77652	Angiogene
	34	20	100.0	20	6 ABS78275	Angiogene
C	35	20	100.0	20	6 ABL38700	Immunosti
	36	20	100.0	20	6 ABL39189	Immunosti
	37	20	100.0	20	6 ABK46426	Immunosti
	38	20	100.0	20	6 AAL44491	CpG motif
	39	20	100.0	20	6 AAL39221	Murine To
	40	20	100.0	20	6 ABS70562	Dendritic
	41	20	100.0	20	6 ABS70554	Dendritic
	42	20	100.0	20	8 ABX89850	Cancer me
	43	20	100.0	20	9 ACA92706	Immunosti
	44	20	100.0	20	9 ACD91416	Immunosti
	45	20	100.0	20	9 ACH03097	Immunosti

ALIGNMENTS

RESULT 1	
AAV60952	
ID AAV60952 standard; DNA; 20 BP.	
XX	
AC AAV60952;	
XX	
DT 14-DEC-1998 (first entry)	
XX	
DE	Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 3.
DE	ss: unmethylated CpG dinucleotide; immune response; natural killer cell;
KW	Th2 response; Th1 response; Th1 cytokine; hepatitis B.
KW	
XX	Synthetic.
OS	
XX	
PN WO9840100-A1.	
XX	
PD 17-SEP-1998.	
XX	
PF 10-MAR-1998; 98WO-US004703.	
XX	
PR 10-MAR-1997; 97US-0040376P.	
XX	
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.	
PA (QIAG-) QIAGEN GMBH.	
PA (IOWA) UNIV IOWA RES FOUND.	
PI Davis HL, Schorr J, Krieg AM;	
XX WPI; 1998-520792/44.	
DR	Use of oligonucleotides containing an unmethylated CpG dinucleotide -
XX	useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
PT	for inducing immune response in subject.
PT	
XX	Disclosure; Page 12; 67pp; English.
PS	
XX	Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
CC	affect the immune response in a subject by activating natural killer
CC	cells or redirecting a subject's immune response from a Th2 to a Th1
CC	response by inducing monocytic and other cells to produce Th1 cytokines.
CC	These nucleic acids containing at least 1 unmethylated CpG can be used as
CC	an adjuvant, specifically to induce an immune response against an
CC	antigenic protein, and are used particularly for virally mediated

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 / Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20
Sequence: 1 tccatgtcgttctctgatgct 20

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A-COMB.seq:
2: /cgn2_6/prodata/1/ina/5B-COMB.seq:
3: /cgn2_6/prodata/1/ina/6A-COMB.seq:
4: /cgn2_6/prodata/1/ina/6B-COMB.seq:
5: /cgn2_6/prodata/1/ina/6C-COMB.seq:
6: /cgn2_6/prodata/1/ina/6D-COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	3	US-08-738-652-43
2	20	100.0	20	3	US-08-738-652-53
3	20	100.0	20	3	US-09-030-701-5
4	20	100.0	20	3	US-09-286-098-48
5	20	100.0	20	3	US-09-286-098-56
6	20	100.0	20	3	US-09-286-098-57
7	20	100.0	20	3	US-08-960-774-38
8	20	100.0	20	3	US-09-082-6498-71
9	20	100.0	20	4	US-09-325-193A-49
10	20	100.0	20	4	US-09-191-170-43
11	20	100.0	20	4	US-09-191-170-51
12	20	100.0	20	4	US-09-337-619-38
13	19	95.0	20	3	US-09-030-701-25
14	19	95.0	20	3	US-08-960-774-44
15	19	95.0	20	3	US-09-082-6498-72
16	19	95.0	20	4	US-09-337-619-44
17	18.4	92.0	20	1	US-08-436-714-7
18	18.4	92.0	20	1	US-08-442-705-7
19	18.4	92.0	20	1	US-08-332-829-7
20	18.4	92.0	20	2	US-09-133-774-11
21	18.4	92.0	20	3	US-08-386-063-21
22	18.4	92.0	20	3	US-08-386-063-25
23	18.4	92.0	20	3	US-09-303-862-11
24	18.4	92.0	20	3	US-08-386-063-21
25	18.4	92.0	20	3	US-08-386-063-25
26	18.4	92.0	20	3	US-08-738-652-7
27	18.4	92.0	20	3	US-08-738-652-31

28	18.4	92.0	20	3	US-08-738-652-33	Sequence 33, Appl
29	18.4	92.0	20	3	US-08-738-652-34	Sequence 34, Appl
30	18.4	92.0	20	3	US-08-738-652-35	Sequence 35, Appl
31	18.4	92.0	20	3	US-08-738-652-37	Sequence 37, Appl
32	18.4	92.0	20	3	US-08-738-652-41	Sequence 41, Appl
33	18.4	92.0	20	3	US-08-738-652-42	Sequence 42, Appl
34	18.4	92.0	20	3	US-08-738-652-44	Sequence 44, Appl
35	18.4	92.0	20	3	US-08-738-652-54	Sequence 54, Appl
36	18.4	92.0	20	3	US-09-030-701-4	Sequence 4, Appl
37	18.4	92.0	20	3	US-09-286-098-22	Sequence 22, Appl
38	18.4	92.0	20	3	US-09-286-098-23	Sequence 23, Appl
39	18.4	92.0	20	3	US-09-286-098-24	Sequence 24, Appl
40	18.4	92.0	20	3	US-09-286-098-42	Sequence 42, Appl
41	18.4	92.0	20	3	US-09-286-098-46	Sequence 46, Appl
42	18.4	92.0	20	3	US-09-286-098-47	Sequence 47, Appl
43	18.4	92.0	20	3	US-08-960-774-28	Sequence 28, Appl
44	18.4	92.0	20	3	US-08-960-774-28	Sequence 28, Appl
45	18.4	92.0	20	3	US-08-960-774-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-08-738-652-43
; Sequence 43, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-43

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCATGTCGTTCTCTGATGCT 20
|||
Db 1 TCCATGTCGTTCTCTGATGCT 20

RESULT 2

US-08-738-652-53
; Sequence 53, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgtcgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	9	US-09-824-468-48
2	20	100.0	20	9	US-09-824-468-56
3	20	100.0	20	9	US-09-824-468-57
4	20	100.0	20	9	US-09-800-266A-49
5	20	100.0	20	9	US-09-895-007A-49
6	20	100.0	20	9	US-09-920-313-49
7	20	100.0	20	10	US-09-888-326-62
8	20	100.0	20	10	US-09-888-326-611
9	20	100.0	20	10	US-09-818-918-43
10	20	100.0	20	10	US-09-818-918-53
11	20	100.0	20	10	US-09-931-583-57
12	20	100.0	20	10	US-09-776-479-136

13	20	100.0	20	10	US-09-776-479-759	Sequence 759, App
14	20	100.0	20	10	US-09-954-987B-96	Sequence 96, Appl
15	20	100.0	20	10	US-09-967-464-6	Sequence 6, Appl
16	20	100.0	20	11	US-09-874-991C-43	Sequence 43, Appl
17	20	100.0	20	11	US-09-874-991C-109	Sequence 109, App
18	20	100.0	20	11	US-09-874-991C-132	Sequence 132, App
19	20	100.0	20	11	US-09-874-991C-160	Sequence 160, App
20	20	100.0	20	11	US-09-874-991C-181	Sequence 181, App
21	20	100.0	20	11	US-09-874-991C-206	Sequence 206, App
22	20	100.0	20	11	US-09-874-991C-422	Sequence 422, App
23	20	100.0	20	11	US-09-874-991C-441	Sequence 441, App
24	20	100.0	20	11	US-09-776-479-136	Sequence 136, App
25	20	100.0	20	11	US-09-776-479-759	Sequence 759, App
26	20	100.0	20	11	US-09-965-101-71	Sequence 71, Appl
27	20	100.0	20	13	US-10-023-909A-49	Sequence 49, Appl
28	20	100.0	20	13	US-10-074-956-2	Sequence 2, Appl
29	20	100.0	20	14	US-10-112-653-8	Sequence 8, Appl
30	20	100.0	20	14	US-10-112-653-129	Sequence 129, App
31	20	100.0	20	14	US-10-112-653-732	Sequence 732, App
32	20	100.0	20	14	US-10-017-995-136	Sequence 136, App
33	20	100.0	20	14	US-10-017-995-759	Sequence 759, App
34	20	100.0	20	14	US-10-300-247-49	Sequence 49, Appl
35	20	100.0	20	15	US-10-161-229-43	Sequence 43, Appl
36	20	100.0	20	15	US-10-187-264A-38	Sequence 38, Appl
37	20	100.0	20	15	US-10-265-072-94	Sequence 94, Appl
38	20	100.0	20	15	US-10-306-522-38	Sequence 38, Appl
39	20	100.0	20	15	US-10-314-578-136	Sequence 136, App
40	20	100.0	20	15	US-10-314-578-759	Sequence 759, App
41	20	100.0	20	15	US-10-434-696-49	Sequence 49, Appl
42	20	100.0	20	16	US-10-373-381-43	Sequence 43, Appl
43	20	100.0	20	16	US-10-373-381-44	Sequence 44, Appl
44	20	100.0	20	16	US-10-719-493-38	Sequence 38, Appl
45	20	100.0	20	17	US-10-627-331-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-824-468-48
; Sequence 48, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-48

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGTCGTCCTCATGCT 20

DB 1 TCCATGTCGTCCTCATGCT 20

RESULT 2

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgccttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	18.4	92.0	70	1	AA855652	vw70g01.r
C 2	18.4	92.0	97	1	AA082589	zn23309.r
C 3	18.4	92.0	287	2	BF713668	ESTPBL223
C 4	18.4	92.0	435	5	BY253224	BY253224
C 5	18.4	92.0	461	8	AZ721917	RPCI-24-1
C 6	18.4	92.0	484	4	B1899835	ib66d01.y
C 7	18.4	92.0	490	5	BU572806	PA_Ea000
C 8	18.4	92.0	520	6	CA573700	K05G04E04
C 9	18.4	92.0	522	6	CA547142	K0143B06
C 10	18.4	92.0	532	6	CA545112	K0108B06
C 11	18.4	92.0	539	5	BU575237	PA_Ea000
C 12	18.4	92.0	556	8	AZ752416	RPCI-24-6
C 13	18.4	92.0	571	8	AZ023370	RPCI-23-3
C 14	18.4	92.0	575	5	BU574826	PA_Ea000
C 15	18.4	92.0	578	4	BM730295	ih62g03.y
C 16	18.4	92.0	585	5	BP767484	BP767484
C 17	18.4	92.0	592	8	AZ985535	2M0267K19
C 18	18.4	92.0	608	4	B1100477	602886587
C 19	18.4	92.0	630	4	B1330822	602981204
C 20	18.4	92.0	636	2	BB654216	BB654216
C 21	18.4	92.0	637	4	BG863609	602796816
C 22	18.4	92.0	638	4	B1329902	602980033
C 23	18.4	92.0	642	2	BP229738	602029243
C 24	18.4	92.0	646	2	BE368574	601220573

C 25	18.4	92.0	649	5	BP765421	BP765421
C 26	18.4	92.0	669	2	BE290326	601089294
C 27	18.4	92.0	674	6	CF169634	B0816C03
C 28	18.4	92.0	679	8	AZ837234	2M013J20
C 29	18.4	92.0	684	4	BG862940	60297636
C 30	18.4	92.0	685	4	BG974078	60284370
C 31	18.4	92.0	689	5	BU613249	UI-M-EMO-
C 32	18.4	92.0	700	5	BM944939	UI-M-EMO-
C 33	18.4	92.0	702	7	CF739812	UI-M-EMO-
C 34	18.4	92.0	705	6	CA317115	UI-M-EMO-
C 35	18.4	92.0	713	6	CA319143	UI-M-FW0-
C 36	18.4	92.0	727	8	AZ915252	RPCI-24-1
C 37	18.4	92.0	730	4	BI904426	603168092
C 38	18.4	92.0	731	6	CB950574	ACENCOURT
C 39	18.4	92.0	734	6	CB948065	ACENCOURT
C 40	18.4	92.0	735	6	CB948157	ACENCOURT
C 41	18.4	92.0	737	8	AZ901548	RPCI-24-1
C 42	18.4	92.0	738	4	BG862224	602795825
C 43	18.4	92.0	741	8	BH057351	RPCI-24-3
C 44	18.4	92.0	743	4	BI695125	603345256
C 45	18.4	92.0	746	4	BI147210	602913118

ALIGNMENTS

RESULT 1
AA855652/c
LOCUS
DEFINITION
vw70g01.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1260336 5' similar to gb:M11301 Mouse (MOUSE);, mRNA
sequence.
ACCESSION
AA855652
VERSION
AA855652.1 GI:2943190
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 70)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info:image.lnl.gov) for further information.
MGI:662888
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 19.
Location/Qualifiers
1..70
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1260336"
/sex="pooled"
/tissue_type="heart"
/dev_stages="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 461.774 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6	100.0	6	6	CQ801400	Sequence
2	6	100.0	6	6	AX104952	Sequence
3	6	100.0	6	6	AX155589	Sequence
4	6	100.0	6	6	AX465334	Sequence
5	6	100.0	6	6	BD069960	Use of nu
6	6	100.0	7	6	BD267915	Methods f
7	6	100.0	7	6	AX455643	Sequence
8	6	100.0	7	6	AX465336	Sequence
9	6	100.0	7	6	BD013729	Method of
10	6	100.0	7	6	BD069928	Use of nu
11	6	100.0	8	6	E40310	Polynucleot
12	6	100.0	8	6	E40311	Polynucleot
13	6	100.0	8	6	E40312	Polynucleot
14	6	100.0	8	6	AX104953	Sequence
15	6	100.0	8	6	AX114123	Sequence
16	6	100.0	8	6	BD013682	Method of
17	6	100.0	8	6	BD017097	Substrate
18	6	100.0	10	6	BD240666	Preparati
19	6	100.0	10	6	E64719	Method for

C 20	6	100.0	10	6	AR222986	Sequence
C 21	6	100.0	10	6	AR303697	Sequence
C 22	6	100.0	10	6	AR303705	Sequence
C 23	6	100.0	10	6	AX153052	Sequence
C 24	6	100.0	10	6	AX362616	Sequence
C 25	6	100.0	10	6	BD065105	Character
C 26	6	100.0	10	6	BD091161	PSJ-induc
C 27	6	100.0	11	6	BD174616	Modified
C 28	6	100.0	11	6	CQ776205	Sequence
C 29	6	100.0	11	6	CQ776221	Sequence
C 30	6	100.0	11	6	CQ776284	Sequence
C 31	6	100.0	11	6	CQ833423	Sequence
C 32	6	100.0	11	6	AX625408	Sequence
C 33	6	100.0	11	6	AX626514	Sequence
C 34	6	100.0	11	6	AX630376	Sequence
C 35	6	100.0	11	9	S83243	CF transmem
C 36	6	100.0	12	6	A30298	Synthetic I
C 37	6	100.0	12	6	A91493	Sequence 20
C 38	6	100.0	12	6	AR021360	Sequence
C 39	6	100.0	12	6	AR042922	Sequence
C 40	6	100.0	12	6	AR084615	Sequence
C 41	6	100.0	12	6	AR161214	Sequence
C 42	6	100.0	12	6	AR167667	Sequence
C 43	6	100.0	12	6	BD181343	Method of
C 44	6	100.0	12	6	BD181357	Method of
C 45	6	100.0	12	6	BD184693	Method of

ALIGNMENTS

RESULT 1
CQ801400
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CQ801400
Sequence 13 from Patent WO2004032958.
CQ801400
CQ801400.1 GI:47058061
unidentified
unidentified
unclassified.
1
Pizza,M.C.
Polypeptide-vaccines for broad protection against hypervirulent
meningococcal lineages
Patent: WO 2004032958-A 13 22-APR-2004;
Chiron SRL (IT)
Location/Qualifiers
1..6
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="CpG motif"

linear PAT 05-MAY-2004

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGTT 6
Db 1 GTCGTT 6

RESULT 2

AX104952
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX104952
Sequence 1144 from Patent WO0122972.
AX104952
AX104952.1 GI:13921149
synthetic construct
synthetic construct

linear PAT 30-APR-2001

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 70.1887 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	6	ABK46412
2	6	100.0	6	6	ABK46412
3	6	100.0	6	12	ADO04784
4	6	100.0	7	6	ABK46414
5	6	100.0	7	6	ABK46414
6	6	100.0	7	12	ADO04829
7	6	100.0	9	2	AAV09830
8	6	100.0	9	12	ADI16090
9	6	100.0	10	2	AAV50085
10	6	100.0	10	2	AAV35921
11	6	100.0	10	2	AAV5921
12	6	100.0	10	3	AAV5921
13	6	100.0	10	3	AAV5921
14	6	100.0	10	3	AAV5921
15	6	100.0	10	3	AAV5921
16	6	100.0	10	3	AAV5921
17	6	100.0	10	3	AAV5921
18	6	100.0	10	3	AAV5921
19	6	100.0	10	3	AAV5921
20	6	100.0	10	5	AAV5921
21	6	100.0	10	5	AAV5921

22	6	100.0	10	5	AAF33302
23	6	100.0	10	5	AAF33302
24	6	100.0	10	5	AAF33302
25	6	100.0	10	5	AAF33302
26	6	100.0	10	5	AAF33302
27	6	100.0	10	5	AAF33302
28	6	100.0	10	5	AAF33302
29	6	100.0	10	5	AAF33302
30	6	100.0	10	5	AAF33302
31	6	100.0	10	5	AAF33302
32	6	100.0	10	5	AAF33302
33	6	100.0	10	5	AAF33302
34	6	100.0	10	5	AAF33302
35	6	100.0	10	5	AAF33302
36	6	100.0	10	5	AAF33302
37	6	100.0	10	5	AAF33302
38	6	100.0	10	5	AAF33302
39	6	100.0	10	5	AAF33302
40	6	100.0	10	5	AAF33302
41	6	100.0	10	5	AAF33302
42	6	100.0	10	5	AAF33302
43	6	100.0	10	5	AAF33302
44	6	100.0	10	5	AAF33302
45	6	100.0	10	5	AAF33302

ALIGNMENTS

RESULT 1

ABK46412

ID ABK46412 standard; DNA; 6 BP.

XX

AC ABK46412;

DT 05-JUN-2002 (first entry)

XX

DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #2.

XX

KW unmethylated CpG; oligodeoxynucleotide; ON; virucide; vaccine;

KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX

OS Synthetic.

XX

PN WO200211761-A2.

XX

PD 14-FEB-2002.

XX

PF 09-AUG-2001; 2001WO-US041633.

XX

PR 10-AUG-2000; 2000US-0224011P.

XX

PA 01-SEP-2000; 2000US-0229307P.

XX

PI (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX

PI Mond JJ, Prince G, Kliman DM;

XX

DR WPI; 2002-227118/28.

XX

PT Vaccine for immunizing patient against respiratory syncytial virus, has

PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

XX

PT linked by phosphate bond-oligodeoxynucleotides.

XX

PS Claim 4; Page 7; 30pp; English.

XX

CC The invention describes a vaccine comprising one or more epitopes of a

CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by

CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of

CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

CC primary cause of viral bronchiolitis and pneumonia in infants and

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 13.4717 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcggt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	3	US-09-030-701-49
2	6	100.0	6	3	US-08-960-774-57
3	6	100.0	6	4	US-09-325-193A-95
4	6	100.0	6	4	US-09-347-343-24
5	6	100.0	6	4	US-09-337-619-57
6	6	100.0	7	3	US-09-030-701-17
7	6	100.0	7	4	US-09-325-193A-97
8	6	100.0	7	4	US-09-337-619-102
9	6	100.0	8	1	US-07-949-541A-5
10	6	100.0	8	1	US-07-949-541A-9
11	6	100.0	8	1	US-07-949-541A-14
12	6	100.0	8	3	US-09-527-234A-2
13	6	100.0	8	3	US-09-527-234A-2
14	6	100.0	8	4	US-09-527-233B-2
15	6	100.0	10	4	US-09-154-750A-39
16	6	100.0	10	4	US-09-508-753B-422
17	6	100.0	10	4	US-09-508-753B-422
18	6	100.0	12	1	US-08-053-131-8
19	6	100.0	12	1	US-08-645-641-8
20	6	100.0	12	1	US-07-853-408B-8
21	6	100.0	12	1	US-08-096-762-8
22	6	100.0	12	2	US-08-308-865-8
23	6	100.0	12	2	US-08-613-965-6
24	6	100.0	12	2	US-08-918-966-6
25	6	100.0	12	3	US-08-921-655-6
26	6	100.0	12	3	US-09-042-353-160
27	6	100.0	12	3	US-09-281-418-31

C 28	6	100.0	12	3	US-08-758-417A-8	Sequence 8, Appli
C 29	6	100.0	12	5	PT-US92-10983-8	Sequence 8, Appli
C 30	6	100.0	13	3	US-09-336-228B-9	Sequence 9, Appli
C 31	6	100.0	13	3	US-09-030-701-56	Sequence 56, Appli
C 32	6	100.0	13	3	US-09-286-098-98	Sequence 98, Appli
C 33	6	100.0	13	3	US-08-960-774-85	Sequence 85, Appli
C 34	6	100.0	13	4	US-09-325-193A-84	Sequence 84, Appli
C 35	6	100.0	13	4	US-09-191-170-92	Sequence 92, Appli
C 36	6	100.0	13	4	US-08-862-629B-6	Sequence 6, Appli
C 37	6	100.0	13	4	US-08-862-629B-7	Sequence 7, Appli
C 38	6	100.0	13	4	US-08-862-629B-8	Sequence 8, Appli
C 39	6	100.0	13	4	US-09-083-235A-6	Sequence 6, Appli
C 40	6	100.0	13	4	US-09-083-235A-7	Sequence 7, Appli
C 41	6	100.0	13	4	US-09-083-235A-8	Sequence 8, Appli
C 42	6	100.0	13	4	US-09-337-619-85	Sequence 85, Appli
C 43	6	100.0	14	1	US-08-366-783-10	Sequence 10, Appli
C 44	6	100.0	14	1	US-08-834-776A-5	Sequence 5, Appli
C 45	6	100.0	14	3	US-09-078-283A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-030-701-49

; Sequence 49, Application US/09030701B

; Patent No. 6214806

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Schwartz, David A.

; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING

; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF

; FILE REFERENCE: C1039/7011

; CURRENT APPLICATION NUMBER: US/09/030,701B

; PRIOR FILING DATE: 1998-02-25

; PRIOR FILING DATE: 1997-02-28

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 49

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide

; US-09-030-701-49

Query Match 100.0%; Score 6; DB 3; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.1e+08;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGTT 6

Db 1 GTCGTT 6

RESULT 2

US-08-960-774-57

; Sequence 57, Application US/08960774

; Patent No. 6239116

; GENERAL INFORMATION:

; APPLICANT: Krieg et al.,

; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 60.9057 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8185004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	10	US-09-954-987B-66
2	6	100.0	6	13	US-10-023-909A-95
3	6	100.0	6	14	US-10-300-247-97
4	6	100.0	6	15	US-10-253-117-24
5	6	100.0	6	15	US-10-187-264A-57
6	6	100.0	6	15	US-10-306-522-102
7	6	100.0	6	15	US-10-314-578-1145
8	6	100.0	6	15	US-10-434-696-97
9	6	100.0	6	16	US-10-719-493-57
10	6	100.0	6	17	US-10-627-331-102
11	6	100.0	6	18	US-10-757-345-49
12	6	100.0	6	18	US-10-757-345-167

13	6	100.0	7	10	US-09-954-987B-120	Sequence 120, Appl
14	6	100.0	7	13	US-10-023-909A-97	Sequence 97, Appl
15	6	100.0	7	14	US-10-300-247-97	Sequence 97, Appl
16	6	100.0	7	15	US-10-187-264A-102	Sequence 102, Appl
17	6	100.0	7	15	US-10-306-522-102	Sequence 102, Appl
18	6	100.0	7	15	US-10-434-696-97	Sequence 97, Appl
19	6	100.0	7	16	US-10-719-493-102	Sequence 102, Appl
20	6	100.0	7	17	US-10-627-331-102	Sequence 102, Appl
21	6	100.0	7	18	US-10-757-345-48	Sequence 48, Appl
22	6	100.0	8	13	US-10-034-075-22	Sequence 2, Appl
23	6	100.0	8	15	US-10-314-578-1145	Sequence 1145, Ap
24	6	100.0	8	18	US-10-757-345-47	Sequence 47, Appl
25	6	100.0	9	18	US-10-613-524-4	Sequence 4, Appl
26	6	100.0	10	9	US-09-154-750A-39	Sequence 39, Appl
27	6	100.0	10	13	US-10-033-145-2084	Sequence 2084, Ap
28	6	100.0	10	15	US-10-330-627-967	Sequence 967, Appl
29	6	100.0	10	18	US-10-613-524-26	Sequence 26, Appl
30	6	100.0	10	18	US-10-816-220-429	Sequence 429, Appl
31	6	100.0	11	16	US-10-279-684A-33	Sequence 33, Appl
32	6	100.0	11	18	US-10-613-524-25	Sequence 25, Appl
33	6	100.0	11	18	US-10-757-345-26	Sequence 26, Appl
34	6	100.0	11	18	US-10-757-345-46	Sequence 46, Appl
35	6	100.0	11	18	US-10-757-345-159	Sequence 159, Appl
36	6	100.0	12	9	US-09-877-526A-36	Sequence 36, Appl
37	6	100.0	12	9	US-09-877-526A-38	Sequence 38, Appl
38	6	100.0	12	10	US-09-992-160-36	Sequence 36, Appl
39	6	100.0	12	10	US-09-992-160-38	Sequence 38, Appl
40	6	100.0	12	14	US-10-056-761-36	Sequence 36, Appl
41	6	100.0	12	14	US-10-056-761-38	Sequence 38, Appl
42	6	100.0	12	15	US-10-217-106-99	Sequence 99, Appl
43	6	100.0	12	15	US-10-217-106-100	Sequence 100, Appl
44	6	100.0	12	15	US-10-237-016-91	Sequence 91, Appl
45	6	100.0	12	15	US-10-237-016-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1

US-09-954-987B-66
; Sequence 66, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AWS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-954-987B-66

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 796.019 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	6	100.0	15	9 AJ587442	AJ587442 Arabidops
C 2	6	100.0	16	9 AJ52989	AJ52989 Arabidops
C 3	6	100.0	18	4 BM37867	BM37867 5009-0-38
C 4	6	100.0	19	4 BM401163	BM401163 5009-0-83
C 5	6	100.0	19	8 AZ595242	AZ595242 1M0407C15
C 6	6	100.0	19	8 AZ595242	AZ595242 1M0407C15
C 7	6	100.0	20	9 AJ587844	AJ587844 Arabidops
C 8	6	100.0	21	4 BM398235	BM398235 5009-0-42
C 9	6	100.0	22	1 AA921198	AA921198 v227f12.1
C 10	6	100.0	22	1 AJ088271	AJ088271 qa86g08.s
C 11	6	100.0	23	1 AJ790638	AJ790638 AJ790638
C 12	6	100.0	23	8 AZ308993	AZ308993 1M0012M04
C 13	6	100.0	23	8 AZ829494	AZ829494 2M0107N09
C 14	6	100.0	23	8 BH848405	BH848405 SALK_0681
C 15	6	100.0	23	9 AJ600996	AJ600996 Arabidops
C 16	6	100.0	24	4 BM401014	BM401014 5009-0-81
C 17	6	100.0	24	6 CF339314	CF339314 RCL1--04-
C 18	6	100.0	24	6 CF339742	CF339742 RCL1--05-
C 19	6	100.0	24	8 AZ374821	AZ374821 1M0127G19
C 20	6	100.0	24	8 AZ474821	AZ474821 1M0292A16
C 21	6	100.0	24	8 BH857694	BH857694 SALK_0161
C 22	6	100.0	24	9 TA201F10P	TA201F10P
C 23	6	100.0	25	1 AI000280	AI000280 ov10e04.s
C 24	6	100.0	25	1 AI638719	AI638719 tt24e01.x

C 25	6	100.0	25	8 BH906076	BH906076 SALK_1091
C 26	6	100.0	25	8 BZ383367	BZ383367 SALK_1338
C 27	6	100.0	25	8 CC455475	CC455475 SALK_0825
C 28	6	100.0	25	9 CG708827	CG708827 119010G1
C 29	6	100.0	26	8 CA587202	CA587202 LBE09p60
C 30	6	100.0	26	8 BH789316	BH789316 SALK_0190
C 31	6	100.0	26	8 BH909213	BH909213 SALK_0524
C 32	6	100.0	27	5 BX555323	BX555323 BX555323
C 33	6	100.0	27	5 BX555323	BX555323 BX555323
C 34	6	100.0	27	9 TAILH06Q	TAILH06Q
C 35	6	100.0	27	9 TA274G1P	TA274G1P
C 36	6	100.0	27	9 AG187895	AG187895 Pan trogl
C 37	6	100.0	27	9 AG198308	AG198308 Pan trogl
C 38	6	100.0	28	1 AI641251	AI641251 fc21a06.x
C 39	6	100.0	28	1 AJ794924	AJ794924 8B73107.y
C 40	6	100.0	28	5 BX555317	BX555317 BX555317
C 41	6	100.0	28	6 CF340587	CF340587
C 42	6	100.0	28	8 AZ863855	AZ863855 2M0173H11
C 43	6	100.0	28	9 AJ590490	AJ590490 Arabidops
C 44	6	100.0	29	6 CF281394	CF281394 14ETL--08
C 45	6	100.0	29	8 AQ025665	AQ025665 1(2)07864

ALIGNMENTS

RESULT 1
AJ587442/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 278F02, genomic survey sequence.
ACCESSION
AJ587442
VERSION
1 GI:37937066
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE
AUTHORS
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Leclercq, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 15)
AUTHORS
Balzergue, S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Crémieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbio.fr>).
FEATURES
source
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone="278F02"
misc_feature
1..15
misc_lib="Arabidopsis thaliana T-DNA insertion lines"